

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:26 ; Search time 19 Seconds
(without alignments)
35.448 Million cell updates/sec

Title: US-09-910-582B-2

Perfect score: 44

Sequence: 1 GGGVFWQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	47.7	7	2	S33567 tubulin beta-3 cha
2	19	43.2	6	2	B35640 cerebellar degener
3	18	40.9	5	2	C53284 T-cell receptor be
4	18	40.9	7	2	E61491 seed protein ws-5
5	17	38.6	5	2	JH0253 gut pentapeptide -
6	17	38.6	7	2	S21230 dermorphin (Trp-4,
7	16	36.4	7	4	S15597 orf 4 rara 5'-regi
8	15	34.1	6	2	S66195 alcohol dehydrogen
9	14	31.8	7	2	S09652 hypothetical prote
10	13	29.5	5	2	PT0308 Ig heavy chain CRD
11	13	29.5	6	2	JN0861 pectidyl-dipeptida
12	13	29.5	6	2	A31263 dihydrofolate redu
13	13	29.5	6	2	B31263 dihydrofolate redu
14	13	29.5	7	2	PT0727 T-cell receptor be
15	13	29.5	7	2	PT0688 T-cell receptor be
16	13	29.5	7	2	S58797 serine/threonine-s
17	13	29.5	7	2	A58512 venom heptapeptide
18	13	29.5	7	4	PC2056 trichodecenen I -
19	13	29.5	7	4	PC2057 trichodecenen II -
20	12	27.3	3	3	A23751 spinal cord peptid
21	12	27.3	4	2	A53284 T-cell receptor be
22	12	27.3	4	2	B53284 T-cell receptor be
23	12	27.3	4	2	S47552 ubiquitin - rat
24	12	27.3	4	2	PT0706 T-cell receptor be
25	12	27.3	5	2	B61445 Leu-enkephalin - b
26	12	27.3	5	2	A61445 Met-enkephalin - b
27	12	27.3	5	2	B61168 cocoonase (EC 3.4.
28	12	27.3	5	2	PT0267 Ig heavy chain CRD
29	12	27.3	5	2	D44823 synaptosomal-assoc

30	12	27.3	5	2	PT0707 T-cell receptor be
31	12	27.3	5	2	PT0669 T-cell receptor be
32	12	27.3	5	2	PT0585 T-cell receptor be
33	12	27.3	5	2	PT0717 T-cell receptor be
34	12	27.3	5	2	C23751 spinal cord peptid
35	12	27.3	6	2	JU0355 lipopeptide WS1279
36	12	27.3	6	2	PT0280 Ig heavy chain CRD
37	12	27.3	6	2	PT0514 T-cell receptor be
38	12	27.3	6	2	PT0512 T-cell receptor be
39	12	27.3	6	2	PT0720 T-cell receptor be
40	12	27.3	6	2	PT0560 T-cell receptor be
41	12	27.3	6	2	PT0723 T-cell receptor be
42	12	27.3	6	2	PT0726 T-cell receptor be
43	12	27.3	6	2	PT0730 T-cell receptor be
44	12	27.3	6	2	A41946 T-cell receptor ga
45	12	27.3	6	2	PT0605 T-cell receptor be
46	12	27.3	7	2	A60224 Met-enkephalin-Arg
47	12	27.3	7	2	S42407 gramicidin S synth
48	12	27.3	7	2	PT0526 T-cell receptor be
49	12	27.3	7	2	PT0523 T-cell receptor be
50	12	27.3	7	2	PT0642 T-cell receptor be
51	12	27.3	7	2	PT0667 T-cell receptor be
52	12	27.3	7	2	PT0666 T-cell receptor be
53	12	27.3	7	2	PT0663 T-cell receptor be
54	12	27.3	7	2	PT0542 T-cell receptor be
55	12	27.3	7	2	PT0683 T-cell receptor be
56	12	27.3	7	2	PT0719 T-cell receptor be
57	12	27.3	7	2	PT0586 T-cell receptor be
58	12	27.3	7	2	PT0702 T-cell receptor be
59	12	27.3	7	2	PT0728 T-cell receptor be
60	12	27.3	7	2	S33244 neuromodulatory pe
61	12	27.3	7	2	S33245 neuromodulatory pe
62	12	27.3	7	2	S33246 neuromodulatory pe
63	11	25.0	3	3	F37196 bradykinin-potenti
64	11	25.0	4	2	A34826 RCH-related neuro
65	11	25.0	4	2	PT0661 T-cell receptor be
66	11	25.0	5	2	A32516 cholecystokinin-5
67	11	25.0	5	2	A60803 neuropeptide - sea
68	11	25.0	5	2	PT0281 Ig heavy chain CRD
69	11	25.0	5	2	PT0729 T-cell receptor be
70	11	25.0	5	2	PT0703 T-cell receptor be
71	11	25.0	5	2	PT0580 T-cell receptor be
72	11	25.0	5	2	G37196 bradykinin-potenti
73	11	25.0	5	2	B34835 dnaA protein - Pse
74	11	25.0	6	2	PT0629 T-cell receptor be
75	11	25.0	6	2	PT0532 T-cell receptor be
76	11	25.0	6	2	PT0519 T-cell receptor be
77	11	25.0	6	2	PT0604 T-cell receptor be
78	11	25.0	6	2	PT0637 T-cell receptor be
79	11	25.0	6	2	PT0641 T-cell receptor be
80	11	25.0	6	2	F41946 T-cell receptor ga
81	11	25.0	6	2	PD0028 pev-kinin 2 - pena
82	11	25.0	6	2	A27696 contraction-inhibi
83	11	25.0	6	2	B27696 contraction-inhibi
84	11	25.0	6	2	A61068 locustakinin - mig
85	11	25.0	6	2	A43129 neuropeptide GNFR
86	11	25.0	6	4	I79564 hypothetical TCl3
87	11	25.0	7	2	PQ0727 H2 class I protein
88	11	25.0	7	2	E48394 glycoprotein compo
89	11	25.0	7	2	E48394 Ig H chain V-D-J r
90	11	25.0	7	2	PT0628 T-cell receptor be
91	11	25.0	7	2	PT0543 T-cell receptor be
92	11	25.0	7	2	PT0722 T-cell receptor be
93	11	25.0	7	2	PT0689 T-cell receptor be
94	11	25.0	7	2	PX0008 glucuronosyltransf
95	11	25.0	7	2	B48394 major fat-globule
96	11	25.0	7	2	PD0029 pev-kinin 1 - pena
97	11	25.0	7	2	PN0649 pullulanase (EC 3
98	11	25.0	7	2	S57274 triacylglycerol li
99	11	25.0	7	2	A61081 tryptophyllin, bas
100	11	25.0	7	4	I55382 hypothetical pepti

ALIGNMENTS

RESULT 1
 S33567
 tubulin beta-3 chain - fruit fly (*Drosophila melanogaster*) (fragment)
 C;Species: *Drosophila melanogaster*
 C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C;Accession: S33567
 R;Hinz, U.; Wolk, A.; Renkawitz-Pohl, R.
 Development 116, 543-554, 1992
 A;Title: Ultrabithorax is a regulator of beta-3 tubulin expression in the *Drosophila* wing
 A;Reference number: S33567; MUID:93170162; PMID:1363225
 A;Accession: S33567
 A;Status: preliminary; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-7 <HIN>
 A;Cross-references: UNIPROT:P08841; EMBL:X68393; NID:g7669; PIDN:CAA48459.1; PID:g437744
 C;Genetics:
 A;Gene: FlyBase:beta-Tub60D
 A;Cross-references: FlyBase:FBgn0003888
 A;Introns: 5/3

 Query Match 47.7%; Score 21; DB 2; Length 7;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 2 GGVFW 6
 | |
 Db 3 GARFW 7

 RESULT 2
 B35640
 cerebellar degeneration-related protein - mouse (fragment)
 C;Species: *Mus musculus* (house mouse)
 C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993
 C;Accession: B35640
 R;Chen, Y.T.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.B.
 Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990
 A;Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal marker
 A;Reference number: A35640; MUID:90222173; PMID:2326268
 A;Accession: B35640
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-6 <CHE>

 Query Match 43.2%; Score 19; DB 2; Length 6;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 5 FWQ 7
 | |
 Db 1 FWE 3

 RESULT 3
 C53284
 T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
 C;Species: *Oryctolagus cuniculus* (domestic rabbit)
 C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C;Accession: C53284
 R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
 Mol. Immunol. 28, 881-888, 1991
 A;Title: Evolutionarily conserved organization and sequences of germline diversity and J
 A;Reference number: A53284; MUID:91342695; PMID:1678859
 A;Accession: C53284
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-5 <HAR>
 A;Cross-references: GB:S60737; NID:g233916; PIDN:AAB19519.1; PID:g233919
 A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBI:P:60740)
 C;Keywords: T-cell receptor

Query Match 40.9%; Score 18; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 GGG 3
 | | |
 Db 3 GGG 5

 RESULT 4
 E61491
 seed protein ws-5 - winged bean (fragment)
 C;Species: *Psophocarpus tetragonolobus* (winged bean)
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
 C;Accession: E61491
 R;Hirano, H.
 J. Protein Chem. 8, 115-130, 1989
 A;Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dime
 A;Reference number: A61491; MUID:89351606; PMID:2765119
 A;Accession: E61491
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-7 <HIR>
 C;Keywords: glycoprotein; seed

 Query Match 40.9%; Score 18; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 GGG 3
 | | |
 Db 5 GGG 7

 RESULT 5
 JH0253
 gut pentapeptide - Japanese eel
 C;Species: *Anguilla japonica* (Japanese eel)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
 C;Accession: JH0253
 R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
 Biochem. Biophys. Res. Commun. 180, 828-832, 1991
 A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.
 A;Reference number: JH0253; MUID:92062113; PMID:1953755
 A;Accession: JH0253
 A;Molecule type: protein
 A;Residues: 1-5 <UES>
 A;Experimental source: gut
 C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric
 , and of the circular muscle of the gastro-intestinal junction.

 Query Match 38.6%; Score 17; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 5 FW 6
 | |
 Db 2 FW 3

 RESULT 6
 S21230
 dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)
 C;Species: *Phyllomedusa bicolor* (two-colored leaf frog)
 C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000
 C;Accession: S21230
 R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.;
 FEBS Lett. 302, 151-154, 1992
 A;Title: Identification and characterization of two dermorphins from skin extracts of the
 A;Reference number: S21152; MUID:92339502; PMID:1633846
 A;Accession: S21230
 A;Status: preliminary

A;Molecule type: protein
A;Residues: 1-7 <MIG>

C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 38.6%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FW 6
||
Db 3 FW 4

RESULT 7

orf 4 rara 5'-region - human
S15597

C;Species: Homo sapiens (man)
C;Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999

C;Accession: S15597

R;Brand, N.J.; Petkovich, M.; Chambon, P.

Nucleic Acids Res. 18, 6799-6806, 1990

A;Title: Characterization of a functional promoter for the human retinoic acid receptor-1

A;Reference number: S15594; MUID:91088249; PMID:2175878

A;Accession: S15597

A;Molecule type: DNA

A;Residues: 1-7 <BRA>

A;Cross-references: EMBL:X56058; NID:g35876

A;Note: this ORF from Fig. 2 is not annotated in GenBank entry HSRARA2, release 111.0

C;Comment: This sequence is not thought to be translated.

C;Genetics:

A;Gene: GDB:RARA

A;Cross-references: GDB:120337; OMIM:180240

A;Map position: 17q12-17q12

Query Match 36.4%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGV 4
||
Db 4 GGV 6

RESULT 8

S66195

alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fragment)

C;Species: Gadus sp. (cod)

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998

C;Accession: S66195

R;Hjelmqvist, L.; Hackett, M.; Shafiqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.;

FEBS Lett. 367, 237-240, 1995

A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. M

zyme.

A;Reference number: S66191; MUID:95313382; PMID:7607314

A;Accession: S66195

A;Molecule type: protein

A;Residues: 1-6 <HJE>

C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 34.1%; Score 15; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VFWQ 7
||
Db 3 VAWG 6

RESULT 9

S09652

hypothetical protein (aacC2 3' region) - Enterobacter cloacae (fragment)

C;Species: Enterobacter cloacae

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 08-Oct-1999
C;Accession: S09652

R;Vliegenthart, J.S.; Ketelaar-van Gaalen, P.A.G.; van de Klundert, J.A.M.

Antimicrob. Agents Chemother. 33, 1153-1159, 1989

A;Title: Nucleotide sequence of the aacC2 gene, a gentamicin resistance determinant invol

A;Reference number: S09651; MUID:90024972; PMID:2552900

A;Accession: S09652

A;Molecule type: DNA

A;Residues: 1-7 <VLI>

A;Cross-references: EMBL:X51534; NID:g40878; PIDN:CAA35914.1; PID:g581034

Query Match 31.8%; Score 14; DB 2; Length 7;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VFW 6
||
Db 2 IIW 4

RESULT 10

PT0308

Ig heavy chain CRD3 region (clone 6-88) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0308

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0308

A;Molecule type: DNA

A;Residues: 1-5 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 29.5%; Score 13; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WQ 7
||
Db 2 WE 3

RESULT 11

JN0861

peptidyl-dipeptidase A inhibitory peptide C111 - striped bonito

C;Species: Sarda orientalis (striped bonito)

C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999

C;Accession: JN0861

R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.

Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993

A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe

A;Reference number: JN0859; MUID:94080036; PMID:7764272

A;Accession: JN0861

A;Molecule type: protein

A;Residues: 1-6 <MAT>

A;Experimental source: liver

C;Comment: The carboxyl end is essential for the protein's expression of angiotensin I-co

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 29.5%; Score 13; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GVF 5
||
Db 1 GVV 3

RESULT 12

A31263
 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum
 C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
 C;Accession: A31263
 R;Peterson, D.S.; Walliker, D.; Wellems, T.E.
 Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
 A;Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
 A;Reference number: A94217; MUID:89057886; PMID:2904149
 A;Accession: A31263
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-6 <PET>
 C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 29.5%; Score 13; DB 2; Length 6;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WQ 7
 |:
 Db 3 WE 4

RESULT 13
 B31263
 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum
 C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
 C;Accession: B31263
 R;Peterson, D.S.; Walliker, D.; Wellems, T.E.
 Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
 A;Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
 A;Reference number: A94217; MUID:89057886; PMID:2904149
 A;Accession: B31263
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-6 <PET>
 C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 29.5%; Score 13; DB 2; Length 6;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WQ 7
 |:
 Db 3 WE 4

RESULT 14
 PT0727
 T-cell receptor beta chain V-D-J region (161-2F) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0727
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0727
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-6 <FEE>
 A;Experimental source: newborn thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 29.5%; Score 13; DB 2; Length 6;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGV 4
 |:
 Db 3 GGL 5

RESULT 15
 PT0688
 T-cell receptor beta chain V-D-J region (140-1D) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0688
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0688
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-7 <FEE>
 A;Experimental source: day 18 fetal thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 29.5%; Score 13; DB 2; Length 7;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGVFW 6
 |:
 Db 3 GDADW 7

Search completed: August 3, 2005, 11:42:31
 Job time : 20 secs

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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:27 ; Search time 88.6667 Seconds
(without alignments)
40.427 Million cell updates/sec

Title: US-09-910-582B-2

Perfect score: 44

Sequence: 1 GGGVFWQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 174

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	36.4	7	2 Q8JE61	Q8JE61 human immun
2	14	31.8	7	2 P82445	P82445 nicotiana t
3	13	29.5	7	1 BRHP CONIM	P58803 conus imper
4	13	29.5	7	1 FAR5_HIRME	P42564 hirudo medi
5	12	27.3	5	1 PAP2_PARMA	P81864 pardachirus
6	12	27.3	5	1 UC22_MAIZE	P80628 zea mays (m
7	12	27.3	7	1 ASCL_ALLAS	P84071 allium asca
8	12	27.3	7	1 WWA1_ACHFUF	P35919 achatina fu
9	12	27.3	7	1 WWA2_ACHFUF	P35920 achatina fu
10	12	27.3	7	1 WWA3_ACHFUF	P35921 achatina fu
11	12	27.3	7	2 Q95945	Q95945 saccharomyc
12	12	27.3	7	2 O55184	O55184 rattus norv
13	12	27.3	7	2 Q63480	Q63480 sepiia offic
14	11	25.0	2	1 GWA_SEPOF	P83570 sepiia offic
15	11	25.0	4	1 OCP3_OCTMI	P58649 octopus min
16	11	25.0	5	1 BRP7_BOTIN	P30425 bothrops in
17	11	25.0	5	1 RE32_LITRU	P82073 litoria rub
18	11	25.0	5	1 UF01_MOUSE	P38639 mus musculu
19	11	25.0	6	1 CIP1_MYTED	P13736 mytilus edu
20	11	25.0	6	1 CIP2_MYTED	P13737 mytilus edu
21	11	25.0	6	1 ET01_LITRU	P82096 litoria rub
22	11	25.0	6	1 FARP_MONEX	P41966 monilezia ex
23	11	25.0	6	1 LOK1_LOCOMI	P41491 locusta mig
24	11	25.0	7	1 TFPY_PACDA	P83455 pachymedusa
25	11	25.0	7	1 TY51_LITRU	P82065 litoria rub
26	11	25.0	7	2 Q9BR74	Q9BR74 homo sapien
27	11	25.0	7	2 Q49223	Q49223 glycine max
28	11	25.0	7	2 Q8KMS9	Q8KMS9 enterobacte
29	11	25.0	7	2 Q8GL00	Q8GL00 borrelia bu
30	11	25.0	7	2 Q8GL04	Q8GL04 borrelia bu
31	10	22.7	6	1 SAPP_SEPOF	P83569 sepiia offic

32	10	22.7	7	1 CCF1_ENTFA	P20104 enterococcu
33	10	22.7	7	2 Q9Y182	Q9Y182 gnatholebia
34	9	20.5	4	1 FYRI_ANTEL	P58706 anthopleura
35	9	20.5	4	1 OCP1_OCTMI	P58648 octopus min
36	9	20.5	5	1 PSK_DAUCA	P58261 daucus caro
37	9	20.5	7	1 CIA_ENTFA	P11932 enterococcu
38	9	20.5	7	1 FARI_HELTI	P41871 hellisoma tr
39	8	18.2	4	1 FFKA_ANTEL	P58705 anthopleura
40	7	15.9	5	1 AL14_CARMA	P81817 carcinus ma
41	7	15.9	5	1 RE11_LITRU	P82070 litoria rub
42	7	15.9	5	1 RE21_LITRU	P82071 litoria rub
43	7	15.9	5	1 RE31_LITRU	P82072 litoria rub
44	7	15.9	7	1 ALL2_CARMA	P81805 carcinus ma
45	7	15.9	7	1 ALL3_CARMA	P81806 carcinus ma
46	7	15.9	7	1 ALL4_CARMA	P81807 carcinus ma
47	7	15.9	7	1 ALL5_CARMA	P81808 carcinus ma
48	7	15.9	7	1 ALL7_CVDPO	P82158 cydia pomon
49	7	15.9	7	1 LANC_CARUI	P36960 carnobacter
50	7	15.9	7	1 PPH2_LYCES	P83379 lycopersico
51	7	15.9	7	1 UN06_PINPS	P81675 pinus pinas
52	7	15.9	7	2 Q9C5B3	Q9C5B3 arabidopsis
53	7	15.9	7	2 O50556	O50556 actinobacil
54	7	15.9	7	2 Q07624	Q07624 rous sarcom
55	6	13.6	3	1 GRWM_HUMAN	P01157 homo sapien
56	6	13.6	4	1 ACHI_ACHFUF	P35904 achatina fu
57	6	13.6	4	1 DCML_PSECH	P19916 pseudomonas
58	6	13.6	4	1 EOSI_HUMAN	P02731 homo sapien
59	6	13.6	4	1 FAR3_HIRME	P42562 hirudo medi
60	6	13.6	4	1 FAR4_HIRME	P42563 hirudo medi
61	6	13.6	4	1 FLRF_HIRME	P42561 hirudo medi
62	6	13.6	4	1 FLRN_ANTEL	P58707 anthopleura
63	6	13.6	4	1 FMRF_MACNI	P01162 macrocallis
64	6	13.6	4	2 Q16047	Q16047 homo sapien
65	6	13.6	5	1 AP21_EISFO	P84182 eisenia foe
66	6	13.6	5	1 EI03_LITRU	P82039 litoria rub
67	6	13.6	5	1 EI04_LITRU	P82100 litoria rub
68	6	13.6	5	1 FARP_ARTTR	P41853 artiopesthi
69	6	13.6	5	1 FARP_CHICK	P83308 gallus gall
70	6	13.6	5	1 SUGA_ACHDO	P19991 acheta dome
71	6	13.6	5	1 TPIS_CANFA	P54714 canis famil
72	6	13.6	5	1 UXA4_CHLTR	P38005 chlamydia t
73	6	13.6	6	1 PYFI_PENMO	P84005 penamycin mon
74	6	13.6	7	1 EI05_LITRU	P82101 litoria rub
75	6	13.6	7	1 FAF1_ASCSU	P31889 ascaris suu
76	6	13.6	7	1 FAF2_ASCSU	P67879 ascaris suu
77	6	13.6	7	1 FAF2_PANRE	P67880 panagrellus
78	6	13.6	7	1 FARI_MACRS	P83274 macrobrachi
79	6	13.6	7	1 FARI_PROCL	P38499 procambarus
80	6	13.6	7	1 FAR2_PROCL	P38498 procambarus
81	6	13.6	7	1 FAR3_HAECH	P81298 haemochus
82	6	13.6	7	1 FAR3_PANRE	P41874 panagrellus
83	6	13.6	7	1 FARA_PANRE	P41875 panagrellus
84	6	13.6	7	1 FARB_CALVO	P41866 calliphora
85	6	13.6	7	1 HY7_PIG	P01153 sus scrofa
86	6	13.6	7	1 IGAO_DACDE	P06294 dactylinum d
87	6	13.6	7	1 MNPI_LEPDE	P42984 leptinotars
88	6	13.6	7	1 UF04_MOUSE	P38642 mus musculu
89	6	13.6	7	1 UH11_RAT	P56576 rattus norv
90	6	13.6	7	2 Q15903	Q15903 homo sapien
91	6	13.6	7	2 Q98866	Q98866 spinacia ol
92	6	13.6	7	2 Q8MFY6	Q8MFY6 taraxacum (
93	6	13.6	7	2 Q07354	Q07354 synechococc
94	6	13.6	7	2 Q34028	Q34028 sphingomona
95	6	13.6	7	2 Q8KMS3	Q8KMS3 klebsiella
96	6	13.6	7	2 Q47029	Q47029 enterobacte
97	6	13.6	7	2 Q47505	Q47505 escherichia
98	6	13.6	7	2 Q8K3H6	Q8K3H6 rattus norv
99	6	13.6	7	2 Q9YQ10	Q9YQ10 transmissib
100	5	11.4	3	1 THYL_BOMOR	P62970 bombina ori

ALIGNMENTS

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RESULT 1
Q8UEB1
ID Q8UEB1 PRELIMINARY; PRT; 7 AA.
AC Q8UEB1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DE Bromoheptapeptide Im.
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Truncated pol protein (Fragment).
GN Name-pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=22056123; PubMed=12060770; DOI=10.1073/pnas.112177799;
RA Beerewinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
RA Hoffmann D., Korn K., Selbig J.;
RT "Diversity and complexity of HIV-1 drug resistance: a bioinformatics
RT approach to predicting phenotype from genotype."
RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
DR EMBL; AF347267; AA32344.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;

Query Match 36.4%; Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WQ 7
Db 6 WQ 7

RESULT 2
P82445
ID P82445 PRELIMINARY; PRT; 7 AA.
AC P82445;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 10 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OC NCBI_TaxID=4097;
[1]
RN SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture."
RL Planta 200:0-0(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL.
CC -1- TISSUE SPECIFICITY: XYLEM.
DR GO; GO:0005618; C:cell wall; IEA.
KW Cell wall.
FT NON TER 7
SQ SEQUENCE 7 AA; 758 MW; 69D2C1E862D1B2A0 CRC64;

Query Match 31.8%; Score 14; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVF 5
Db 4 GHVF 7

RESULT 3
BRHP_CONIM
ID BRHP_CONIM STANDARD; PRT; 7 AA.
AC P58803;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bromoheptapeptide Im.
OS Conus imperialis (Imperial cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OC NCBI_TaxID=35631;
[1]
RN SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RP TISSUE=Venom;
RX MEDLINE=97184108; PubMed=9030520; DOI=10.1074/jbc.272.8.4689;
RA Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,
RA Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,
RA McIntosh J.M.;
RT "A novel post-translational modification involving bromination of
RT tryptophan. Identification of the residue, L-6-bromotryptophan, in
RT peptides from Conus imperialis and Conus radiatus venom."
RL J. Biol. Chem. 272:4689-4698(1997).
CC -1- FUNCTION: Does not elicit gross behavioral symptoms when injected
CC centrally or peripherally in mice.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=853.19; METHOD=ESI; RANGE=1-7; NOTE=Ref.1.
DR PIR; A58512; A58512.
KW Amidation; Bromination; Direct protein sequencing;
KW Pyrrolidone carboxylic acid.
FT DISULFID 2 7
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 6 6 6'-bromotryptophan.
FT MOD_RES 7 7 Cysteine amide.
SQ SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;

Query Match 29.5%; Score 13; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GVFW 6
Db 3 GQAW 6

RESULT 4
FAR5_HIRME
ID FAR5_HIRME STANDARD; PRT; 7 AA.
AC P42564;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRamide-like neuropeptide GGYMRF-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OC NCBI_TaxID=6421;
[1]
RN SEQUENCE.
RP MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 7 7 Phenylalanine amide.
SQ SEQUENCE 7 AA; 858 MW; 69D4068B53387810 CRC64;

Query Match 29.5%; Score 13; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 GGVF 5
| :
Db 1 GGY 4

RESULT 5
PAP2_PAPMA
ID_PAP2_PAPMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea moles sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleiidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea moles sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713 (1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels in
CC membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pardaxin family.
KW Direct protein sequencing; Toxin.
FT NON TER 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 27.3%; Score 12; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGVF 6
| :
Db 1 GFFF 4

RESULT 6
UC22_MAIZE
ID_UC22_MAIZE STANDARD; PRT; 5 AA.
AC P80628;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 474)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005 (1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.1, its MW is: 30.4 kDa.
DR Maize-2DPAGE; P80628; COLEOPTILE.

DR MaizeDB; 123954; -.
KW Direct protein sequencing.
FT NON TER 1
FT NON TER 5
SQ SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;

Query Match 27.3%; Score 12; DB 1; Length 5;
Best Local Similarity 25.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VFWQ 7
| :
Db 1 IFPE 4

RESULT 7
ASCL_ALLAS
ID_ASCL_ALLAS STANDARD; PRT; 7 AA.
AC P84071;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ascalin (Fragment).
OS Allium ascalonicum (Shallot) (Allium cepa var. aggregatum).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
OC Allium.
OX NCBI_TaxID=28911;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Bulb;
RX PubMed=12126728; DOI=10.1016/S0196-9781(02)00032-3;
RA Wang H.X., Ng T.B.;
RT "Ascalin, a new anti-fungal peptide with human immunodeficiency virus
RT type 1 reverse transcriptase-inhibiting activity from shallot bulbs."
RL Peptides 23:1025-1029 (2002).
CC -!- FUNCTION: Has antifungal activity against B.cinerea. Inhibits HIV-
CC 1 reverse transcriptase.
CC -!- MISCELLANEOUS: Inhibits HIV-1 reverse transcriptase with an IC(50)
CC of 10 uM.
KW Direct protein sequencing; Fungicide.
FT NON TER 7
SQ SEQUENCE 7 AA; 712 MW; 687866D87EA6CB30 CRC64;

Query Match 27.3%; Score 12; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GG 2
| :
Db 6 GG 7

RESULT 8
WWAI_ACHFU
ID_WWAI_ACHFU STANDARD; PRT; 7 AA.
AC P35919;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE WWamide-1.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720; DOI=10.1016/0014-5793(93)81458-C;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica."
RL FEBS Lett. 323:104-108 (1993).

CC -i- FUNCTION: Exhibits modulatory effects on the peripheral nervous system. Inhibits activity on a central neuron.
 DR PIR; S33245.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 7 Tryptophan amide.
 SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 27.3%; Score 12; DB 1; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Indels 0; Gaps 0;

Qy 6 WQ 7
 |:
 Db 1 WK 2

RESULT 9
 WWA2 ACHFU STANDARD; PRT; 7 AA.
 ID WWA2 ACHFU STANDARD; PRT; 7 AA.
 AC P35920; 1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Wamide-2.
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Ganglion;
 RX MEDLINE=33265912; PubMed=8495720; DOI=10.1016/0014-5793(93)81458-C;
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
 RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
 ganglia of the African giant snail, Achatina fulica.";
 RL FEBS Lett. 323:104-108(1993).
 DR PIR; S33246; S33246.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 7 Tryptophan amide.
 SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 27.3%; Score 12; DB 1; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WQ 7
 |:
 Db 1 WK 2

RESULT 10
 WWA3 ACHFU STANDARD; PRT; 7 AA.
 ID WWA3 ACHFU STANDARD; PRT; 7 AA.
 AC P35921;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Wamide-3.
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Ganglion;
 RX MEDLINE=93265912; PubMed=8495720; DOI=10.1016/0014-5793(93)81458-C;
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
 RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
 ganglia of the African giant snail, Achatina fulica.";
 RL FEBS Lett. 323:104-108(1993).
 DR PIR; S33244; S33244.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 7 Tryptophan amide.

SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 27.3%; Score 12; DB 1; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WQ 7
 |:
 Db 1 WK 2

RESULT 11
 Q9S945 PRELIMINARY; PRT; 7 AA.
 ID Q9S945 PRELIMINARY; PRT; 7 AA.
 AC Q9S945;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Inside intron 5 (Fragment).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Mitochondrion.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D273-10B;
 RX MEDLINE=81069885; PubMed=6254986;
 RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
 RT "Assembly of the mitochondrial membrane system: Structure and
 nucleotide sequence of the gene coding for subunit 1 of yeast
 cytochrome oxidase.";
 RL J. Biol. Chem. 258:11927-11941(1980).
 DR EMBL; V00694; CAA24066.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match 27.3%; Score 12; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WQ 7
 |:
 Db 4 WK 5

RESULT 12
 O5S184 PRELIMINARY; PRT; 7 AA.
 ID O5S184 PRELIMINARY; PRT; 7 AA.
 AC O5S184;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Orphan receptor TR4-NS (Fragment).
 GN Name=TR4;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=96198747; PubMed=8612486; DOI=10.1210/en.137.5.1562;
 RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
 RA Detera-Wadleigh S.D.;
 RT "Splice variants of rat TR4 orphan receptor: differential expression
 of novel sequences in the 5'-untranslated region and C-terminal
 domain.";
 RL Endocrinology 137:1562-1571(1996).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;
 RX MEDLINE=96299786; PubMed=8661150; DOI=10.1006/geno.1996.0368;
 RA Yoshikawa T., DuPont B.R., Leach R.J., Detera-Wadleigh S.D.;
 RT "New variants of the human and rat nuclear hormone receptor, TR4:
 expression and chromosomal localization of the human gene";
 RL Genomics 35:361-366(1996).
 DR EMBL; U59454; AAB91433.1; --
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER
 SQ SEQUENCE 1 1 1
 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 27.3%; Score 12; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GG 2
 ||
 Db 4 GG 5

RESULT 13

Q63480
 ID Q63480 PRELIMINARY; PRT; 7 AA.
 AC Q63480;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE TR4-NS orphan receptor (Fragment).
 GN Name=TR4;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 SEQUENCE FROM N.A.

RX MEDLINE=96198747; PubMed=8612486; DOI=10.1210/en.137.5.1562;
 RA Yoshikawa T., Makino S., Gao X.M., King G.Q., Chuang D.M.,
 RA Detera-Wadleigh S.D.;
 RT "Splice variants of rat TR4 orphan receptor: differential expression
 of novel sequences in the 5'-untranslated region and C-terminal
 RT domain";
 RL Endocrinology 137:1562-1571(1996).
 DR EMBL; U59125; AAB02827.1; --
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER
 SQ SEQUENCE 1 1 1
 7 AA; 758 MW; 672AA87864005350 CRC64;

Query Match 27.3%; Score 12; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GG 2
 ||
 Db 4 GG 5

RESULT 14

GWA_SEPOF
 ID GWA_SEPOF STANDARD; PRT; 2 AA.
 AC P83570;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Neuropeptide GWA.
 OS Sepia officinalis (Common cuttlefish).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Decapodiformes; Sepioidae; Sepiidae; Sepia.
 OX NCBI_TaxID=6610;
 RN [1]
 SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
 RP TISSUE=Optic lobe;

RX MEDLINE=98100358; PubMed=9437704; DOI=10.1016/S0196-9781(97)00241-6;
 RA Henry J., Favrel P., Boucaud-Camou E.;
 RT "Isolation and identification of a novel Ala-Pro-Gly-Trip-amide-related
 peptide inhibiting the motility of the mature oviduct in the
 RT cuttlefish, Sepia officinalis";
 RL Peptides 18:1469-1474(1997).
 CC -1- FUNCTION: Regulatory neuropeptide with myotropic activity
 CC targeting the distal oviduct. Inhibits the motility of the oviduct
 CC by decreasing tonus, frequency and amplitude of contractions.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI; RANGE=1-2; NOTE=Ref.1.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 2 2
 2 Tryptophan amide.
 SQ SEQUENCE 2 AA; 261 MW; 7378100000000000 CRC64;

Query Match 25.0%; Score 11; DB 1; Length 2;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 W 6
 |
 Db 2 W 2

RESULT 15

OCp3_OCTMI
 ID OCp3_OCTMI STANDARD; PRT; 4 AA.
 AC P58649;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cardioactive peptides Ocp-3/Ocp-4.
 OS Octopus minor (Octopus).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
 OX NCBI_TaxID=89766;
 RN [1]
 SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
 RP TISSUE=Brain;
 RX MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;
 RA Iwakoshi E., Hisada M., Minakata H.;
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
 RT Octopus minor";
 RL Peptides 21:623-630(2000).
 CC -1- FUNCTION: Cardioactive; has both positive chronotropic and
 CC inotropic effects on the heart. Ocp-4 is a 1000 time less active
 CC than Ocp-3.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Ocp-4 has D-Ser instead of L-Ser.
 CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
 KW D-amino acid; Direct protein sequencing; Hormone.
 FT MOD_RES 2 2
 2 D-serine (in form Ocp-4).
 SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 25.0%; Score 11; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 W 6
 |
 Db 3 W 3

Search completed: August 3, 2005, 12:07:37
 Job time : 92.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:27 ; Search time 96.3333 Seconds
(without alignments)

28.104 Million cell updates/sec

Title: US-09-910-582B-2

Perfect score: 44

Sequence: 1 GGGVFWQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 121728

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	7	4	AAB30895 Peptide w
2	44	100.0	7	4	AAB50797 Heart hom
3	32	72.7	7	5	ABG77517 Targettin
4	30	68.2	7	2	AAW69090 Neuronal
5	27	61.4	7	2	AAW10773 Ferritin
6	27	61.4	7	2	AAW48924 Membrane
7	26	59.1	7	7	ADL17233 Phage-dis
8	25	56.8	5	2	AAW58581 Kojibiose
9	25	56.8	7	2	AAW39859 Heavy cha
10	25	56.8	7	2	AAW39874 Heavy cha
11	25	56.8	7	2	AAW39862 Heavy cha
12	25	56.8	7	2	AAW39856 Heavy cha
13	25	56.8	7	2	AAW40897 Leader se
14	25	56.8	7	5	AAU81231 Human trk
15	24	54.5	5	5	AAU86976 Estradiol
16	24	54.5	6	3	AAW24307 Prostata
17	24	54.5	6	7	ADB78553 Rat F997-
18	24	54.5	6	8	ADN88732 Human can
19	24	54.5	6	8	ADQ68126 Cancer re
20	24	54.5	7	2	AAW10805 Ferritin
21	24	54.5	7	4	AAW62835 Amino aci
22	24	54.5	7	5	AAE24737 Yeast Vbe
23	24	54.5	7	5	ABG77610 Targettin
24	23	52.3	6	2	AAW20447 Anti-b-en
25	23	52.3	6	5	AAW49437 Penicilli

26	23	52.3	7	7	ADE78402 Peptide (
27	23	52.3	6	8	ABM79662 Peptide c
28	23	52.3	7	4	AAG62839 Amino aci
29	23	52.3	7	5	AAE24741 Yeast Vbe
30	23	52.3	7	6	AAO23874 Protein t
31	23	52.3	7	7	ADL17111 Phage-dis
32	23	52.3	7	8	ABM79691 HIV Vpr m
33	22	50.0	5	2	AAW41532 Pseudomon
34	22	50.0	5	5	ABJ11441 Human 125
35	22	50.0	5	6	ABU72672 Novel pro
36	22	50.0	5	6	ABJ39336 Human leu
37	22	50.0	5	6	ABJ39336 Human leu
38	22	50.0	5	7	ADK41621 Synthetic
39	22	50.0	5	7	ADK41622 Synthetic
40	22	50.0	5	8	ADL12005 D-peptide
41	22	50.0	5	8	ADO63921 Human 213
42	22	50.0	5	8	AAW93214 Zona Pell
43	22	50.0	6	2	AAW03265 Viral int
44	22	50.0	6	2	AAW87430 Peptide d
45	22	50.0	6	2	AAW87395 Peptide d
46	22	50.0	6	2	AAW87396 Peptide d
47	22	50.0	6	2	AAW18678 Peptide S
48	22	50.0	6	4	AAW62355 S. saliva
49	22	50.0	6	7	ADJ76842 CDR seque
50	22	50.0	6	7	ADK41616 Synthetic
51	22	50.0	6	7	ADK41678 VP072 fib
52	22	50.0	7	1	AAW10088 Sequence
53	22	50.0	7	1	AAW61021 Peptide 1
54	22	50.0	7	2	AAW40895 Leader se
55	22	50.0	7	2	AAW87420 Peptide d
56	22	50.0	7	2	AAW49004 Membrane
57	22	50.0	7	5	ABG77601 Targettin
58	22	50.0	7	7	ADW79644 Parapoxvi
59	22	50.0	7	7	ADW15528 Melanoma
60	22	50.0	7	7	ADK41615 Synthetic
61	22	50.0	7	8	ADP13142 Prion pro
62	22	50.0	7	8	ADP75070 Parapoxvi
63	21	47.7	4	2	AAW71194 Peptide u
64	21	47.7	4	5	ABG77506 Targettin
65	21	47.7	5	2	AAW56251 Inulinase
66	21	47.7	5	4	AAW60684 Pyrococcu
67	21	47.7	5	5	AAW85447 Human col
68	21	47.7	6	2	AAW20451 Anti-b-en
69	21	47.7	6	2	AAW87436 Peptide d
70	21	47.7	6	2	AAW55114 ATCC HB 1
71	21	47.7	6	3	AAW86860 Human hae
72	21	47.7	6	3	AAW86359 Human gen
73	21	47.7	6	4	AAW82651 All-D pep
74	21	47.7	6	5	AAW79534 TCR beta-
75	21	47.7	6	5	AAW79531 TCR beta-
76	21	47.7	6	6	AAW35470 Abeta pep
77	21	47.7	6	6	ABO53504 Novel hum
78	21	47.7	6	8	ADQ37294 Vaccine a
79	21	47.7	7	2	AAW87374 Peptide d
80	21	47.7	7	3	AAW13312 Caenorhab
81	21	47.7	7	4	AAU08364 Antibody
82	21	47.7	7	5	ABG77635 Targettin
83	21	47.7	7	5	ABG77603 Targettin
84	21	47.7	7	5	ABG77643 Targettin
85	21	47.7	7	5	ABG77644 Targettin
86	21	47.7	7	5	ABG77642 Targettin
87	21	47.7	7	5	ABG77641 Targettin
88	21	47.7	7	6	ABJ39365 Human leu
89	21	47.7	7	7	ABO33846 Anti-GPI-
90	21	47.7	7	8	ADP90499 Exemplary
91	21	47.7	7	8	ADL95882 Human pro
92	20	45.5	5	4	AAW70984 Melanocor
93	20	45.5	5	5	AAO15574 Vaccine a
94	20	45.5	5	8	ADG45011 Pentapept
95	20	45.5	5	8	ADH68248 Human G-p
96	20	45.5	6	2	AAW62537 Fibronect
97	20	45.5	6	2	AAW55073 Fibronect
98	20	45.5	6	2	AAW55072 Fibronect

99 20 45.5 6 2 AAR69252 Aar69252 Endotheli
100 20 45.5 6 2 AAW40885 Aaw40885 Leader se

ALIGNMENTS

RESULT 1
AAB30895
ID AAB30895 standard; peptide; 7 AA.
XX
AC AAB30895;
XX
DT 02-APR-2001 (first entry)
XX
DE Peptide which selectively binds to normal cardiac endothelium.
XX
KW Cardiac endothelium; angiogenic factor; vascular endothelium;
KW peripheral vascular disease; cardiovascular disease; angiogenesis;
KW cardiac neovascularisation.

XX Unidentified.
XX WO200075329-A1.
XX 14-DEC-2000.
XX 31-MAY-2000; 2000WO-US014988.
XX 07-JUN-1999; 99US-00327045.
XX (EDWA-) EDWARDS LIFESCIENCES CORP.
PA (BAXT) BAXTER AG.
XX Levine AJ, Mitterer A, Falkner F, Scheiflinger F, Dörner F;
PI WPI; 2001-091212/10.
XX

XX New chimeric molecules having an angiogenic factor linked to a targeting
PT molecule that binds to a vascular endothelium, useful for increasing
PT cardiac neovascularization, or treating peripheral vascular and
PT cardiovascular diseases.

PS Disclosure; Page 27; 67pp; English.

XX AAB30895-99 represent targeting molecules, which are used to produce the
CC chimeric molecules of the invention. AAB30895-98 selectively bind to
CC normal cardiac endothelium. The specification describes a chimeric
CC molecule comprising an angiogenic factor linked to a targeting molecule
CC that specifically binds to a vascular endothelium. The chimeric molecules
CC are useful for treatment of peripheral vascular or cardiovascular
CC diseases. Specifically, they are useful for inducing or inhibiting
CC angiogenesis, for increasing cardiac neovascularisation in ischemic
CC tissue in the peripheral vascular system

XX Sequence 7 AA;

Query Match 100.0%; Score 44; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7
|||
Db 1 GGGVFWQ 7

RESULT 2
AAB50797
ID AAB50797 standard; peptide; 7 AA.

XX AAB50797;
XX 21-MAR-2001 (first entry)
DT

XX Heart homing peptide SEQ ID NO: 2.
DE
XX
KW Heart homing peptide; cardiovascular disease; ischaemic disease;
KW gene therapy.
XX
OS Synthetic.

XX WO200075174-A1.
XX 14-DEC-2000.
XX 31-MAY-2000; 2000WO-US015088.
XX 07-JUN-1999; 99US-00326718.

XX (BURN-) BURNHAM INST.

XX Ruoslahti E, Mackenna DA;

XX WPI; 2001-071059/08.

XX Novel heart homing peptide that selectively homes to normal ischemic and
PT cardiac tissue useful for targeting ischemic tissues for treating
PT ischemic and cardiovascular diseases such as atherosclerosis and
PT restenosis.
XX Claim 2; Page 55; 70pp; English.

XX The present invention provides a number of heart homing peptides which
CC selectively home to cardiac tissue. These can be used in the treatment of
CC cardiovascular and ischemic diseases, such as atherosclerosis, myocardial
CC thrombosis, restenosis, vasculitis, atherosclerotic aneurysms, myocardial
CC hypertrophy, congenital heart diseases, ischemic heart disease and
CC anginas, acquired valvular/endocardial diseases, primary myocardial
CC diseases, cardiac tumours and arrhythmias

XX Sequence 7 AA;

Query Match 100.0%; Score 44; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7
|||
Db 1 GGGVFWQ 7

RESULT 3
ABG77517
ID ABG77517 standard; peptide; 7 AA.

XX ABG77517;

XX 05-NOV-2002 (first entry)

DE Targetting peptide selective for human organ, tissue or cell type #50.

XX Human; cytostatic; antiinflammatory; antidiabetic; cardiovascular;
KW immunomodulator; antibacterial; antiviral; gene therapy; cancer;
KW arthritis; diabetes; inflammatory disease; atherosclerosis;
KW autoimmune disease; bacterial infection; viral infection;
KW cardiovascular disease; degenerative disease.

XX Homo sapiens.

XX WO20020723-A2.

XX 14-MAR-2002.

XX 07-SEP-2001; 2001WO-US028044.

XX 08-SEP-2000; 2000US-0231266P.

PR 17-JAN-2001; 2001US-00765101.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PI Arap W, Pasqualini R;
 XX WPI; 2002-599247/64.
 DR
 XX New targeting peptides identified by phage display, useful for treating a
 PT disease state, e.g. cancer, diabetes, inflammatory disease,
 PT atherosclerosis, autoimmune disease, bacterial or viral infection or
 PT cardiovascular disease.
 XX
 PS Claim 16; Fig 2A; 269pp; English.
 XX
 CC The invention describes an isolated peptide of 100 amino acids or less in
 CC size. The peptide is useful for treating a disease state, e.g. cancer,
 CC arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune
 CC disease, bacterial infection, viral infection, cardiovascular disease or
 CC degenerative disease. This sequence represents a human targeting peptide
 CC selective for human organs, tissues or cell types
 XX
 SQ Sequence 7 AA;
 Query Match 72.7%; Score 32; DB 5; Length 7;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GGVPW 6
 DB |||||
 2 GGIPW 6
 RESULT 4
 AAW69090
 ID AAW69090 standard; peptide; 7 AA.
 XX
 AC AAW69090;
 XX
 DT 05-OCT-1998 (first entry)
 XX
 DE Neuronal NOS binding peptide NBP-45.
 XX
 KW nNOS; neuronal nitric oxide synthase; orphan protein domain; OPD;
 KW protein interaction network; PIN; neurological disease; therapy;
 KW motility disorder; muscular dystrophy; amyotrophic lateral sclerosis;
 KW Huntington's disease; Parkinson's disease; Alzheimer's disease;
 KW Duchenne muscular dystrophy; irritable bowel syndrome.
 XX
 OS Synthetic.
 XX
 PN W09823781-A1.
 XX
 PD 04-JUN-1998.
 XX
 XX 26-NOV-1997; 97WO-US021861.
 XX
 XX 26-NOV-1996; 96US-0031793P.
 PR 15-APR-1997; 97US-0043560P.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX
 XX Li M, Stricker NL, Bredt DS, Christopherson KS;
 PI WPI; 1998-322754/28.
 DR
 XX New peptide ligands that bind specific orphan protein domains and related
 PT nucleic acid - and methods for identifying them in random peptide
 PT libraries, useful for treatment of neurological disease, motility
 PT disorders and muscular dystrophy.
 XX
 PS Disclosure; Fig 3b; 93pp; English.
 XX
 PT

CC This sequence represents a neuronal nitric oxide synthase (nNOS) binding
 CC peptide (NBP), and represents a peptide of the invention. This sequence
 CC was identified using the method of the invention for identifying proteins
 CC that interact with a protein binding domain (orphan protein domain, OPD)
 CC of a first protein (protein interaction network, PIN) comprises: (a)
 CC screening a random peptide library of transformed cells, each containing
 CC a plasmid that includes a laco binding site, an encoding a fusion protein
 CC (FP) of lac repressor DNA binding protein and a specific peptide (the
 CC specific peptide being different in each cell); (b) the cells are lysed
 CC under conditions allowing FP to remain bound to laco; (c) the FP is
 CC contacted with OPD and plasmids encoding a peptide that binds to OPD
 CC isolated; (d) isolated plasmids are sequenced, and nucleic acid and
 CC protein databases scanned to identify proteins that contain the peptide.
 CC These peptides can also be used in a peptide ligand detection system. The
 CC peptides and peptide ligands identified by the ligand detection system,
 CC are used for treatment of neurological disease, motility disorders or
 CC muscular dystrophy (e.g. stroke, amyotrophic lateral sclerosis,
 CC Huntington's, Parkinson's or Alzheimer's diseases. Duchenne muscular
 CC dystrophy or irritable bowel syndrome). The peptides act by inhibiting
 CC interaction between an OPD and proteins to which it normally binds, so
 CC can also be used as reagents and as molecular labels for specific
 CC interacting proteins, e.g. to detect nNOS
 XX
 SQ Sequence 7 AA;
 Query Match 68.2%; Score 30; DB 2; Length 7;
 Best Local Similarity 83.3%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGGVFW 6
 DB |||||
 1 GGGVDW 6
 RESULT 5
 AAW10773
 ID AAW10773 standard; peptide; 7 AA.
 XX
 AC AAW10773;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-NOV-1997 (first entry)
 XX
 XX Ferritin motif #16 important for selective binding affinity.
 DE
 XX
 KW Functional surrogate; analyte; affinity receptor; immunoreactive group;
 KW mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia;
 KW cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin;
 KW pregnancy; infectious disease; ferritin; myosin light chain; troponin;
 KW follicle stimulating hormone; human; growth hormone; immunoglobulin E;
 KW prolactin; parathyroid hormone; placental lactogen; hepatitis antigen;
 KW antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus;
 KW Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen;
 KW carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
 XX
 OS Synthetic.
 XX
 PN W09641172-A1.
 XX
 XX 19-DEC-1996.
 PD
 XX 07-JUN-1996; 96WO-US010498.
 XX
 XX 07-JUN-1995; 95US-00476375.
 XX
 XX (CYTO-) CYTOGEN CORP.
 PA
 XX Lee-Owen FV, Carter JM;
 PI WPI; 1997-077284/07.
 DR
 XX Labelled functional surrogate of an analyte - useful as competitor
 PT molecule in affinity assays, esp. for detecting large macromolecules such

PT as ferritin.
 XX Claim 56; Page 55; 156pp; English.
 XX
 CC This sequence represents a peptide motif derived from ferritin which is
 CC important for selective binding affinity. Peptides containing motifs such
 CC as this may be used as functional surrogates in the conjugate of the
 CC invention. The novel labelled conjugate comprises at least one label
 CC attached to a functional surrogate of an analyte of interest. The
 CC surrogate is capable of competing effectively with the analyte for a
 CC limiting amount of an affinity receptor for the analyte. The conjugate
 CC exhibits an activity that is altered upon interaction with the affinity
 CC receptor and this activity can be measured and related to the amount of
 CC the analyte present in a sample. Functional surrogates such as this have
 CC an immunoreactive group that allows the surrogate to compete effectively
 CC and with the analyte for a limiting amount of its affinity receptor.
 CC Functional surrogates are able to mimic naturally occurring analytes.
 CC They can be labelled for use in standard competitive affinity assays
 CC (esp. homogenous immunoassays) for detecting large macromolecules such as
 CC polypeptides, polysaccharides, polynucleotides, glycoproteins and lipid-
 CC containing macromolecules, as well as small haptens. Typical diagnostic
 CC analytes for detection include cardiac or tumour markers, allergens,
 CC hormones related to fertility-pregnancy or analytes associated with
 CC infectious disease. In particular, the assays are useful for detecting
 CC ferritin, follicle stimulating hormone, human growth hormone,
 CC immunoglobulin E, prolactin, parathyroid hormone, human placental
 CC lactogen, hepatitis antigens or antibodies against them, human chorionic
 CC gonadotropin, human luteinising hormone, cytomegalovirus, Chlamydia,
 CC Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, myoglobin,
 CC myosin light chain, troponin, carcinoembryonic antigen, alpha-
 CC fetoprotein, prostate-specific antigen and CA125 (a tumour marker).
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX

SQ Sequence 7 AA;

Query Match 61.4%; Score 27; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGVFW 6
 || ||
 Db 2 GGSFW 7

RESULT 6
 AAY48924

ID 4 AAY48924 standard; peptide; 7 AA.

XX
 AC AAY48924;

DT 20-MAR-2003 (revised)

DT 10-DEC-1999 (first entry)

XX Membrane dipeptidase-binding ovary homing peptide #12.

XX Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
 KW membrane dipeptidase.

XX Synthetic.

OS Homo sapiens.

XX WO9946284-A2.

PN 16-SEP-1999.

XX 10-MAR-1999; 99WO-US005284.

XX 13-MAR-1998; 98US-00042107.

XX 26-FEB-1999; 99US-00258754.

XX (BURN-) BURNHAM INST.

PI Rajotte D, Pasqualini R, Ruoslahti EI;
 XX WPI; 1999-571717/48.
 XX
 PT New peptides which selectively home to organs or tissues, used for, e.g.
 PT identifying target ligands and for therapy of pathological conditions.
 XX
 PS Example 6; Page 152; 193pp; English.

XX The present invention describes peptides that selectively home to a
 CC tissue or organ. The peptides can be used for identifying an organ or
 CC tissue, for identifying a target molecule expressed by an organ or tissue
 CC or for treating an organ or tissue pathology, where the organ or tissue
 CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,
 CC adrenal gland, liver, and lymph node. The peptide bind to the membrane
 CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are
 CC used in the exemplification of the present invention. (Updated on 20-MAR-
 CC 2003 to correct PR field.)

SQ Sequence 7 AA;

Query Match 61.4%; Score 27; DB 2; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7
 || ||
 Db 1 GGDVWWR 7

RESULT 7
 ADL17233

ID ADL17233 standard; peptide; 7 AA.

XX AC ADL17233;

XX 06-MAY-2004 (first entry)

XX Phage-displayed PDZ2 and PDZ3 binding peptide SEQ ID NO:185.

XX 95 kDa post-synaptic density protein/Discs large/ZO-1 domain;
 KW PSD-95/Discs large/ZO-1 domain; PDZ domain; fusion protein;
 KW phage coat protein; PDZ domain binding peptide; cytostatic; nootropic;
 KW neuroprotective; antiparkinsonian; neuroleptic; antitumour;
 KW immunosuppressive; pulmonary; muscular; gene therapy;
 KW Alzheimer's disease; murine typhus; chronic myeloid leukaemia;
 KW rickettsial disease; neurological disorder; Parkinson's disease;
 KW schizophrenia; X-linked autoimmune enteropathy; tsutsugamushi disease;
 KW fascioscapulohumeral muscular dystrophy; late onset demyelinating disease;
 KW Usher syndrome type 1; USH1; nitric oxide-mediated tissue damage; tumour;
 KW cystic fibrosis.

XX Synthetic.

XX WO2003004604-A2.

XX 16-JAN-2003.

XX 03-JUL-2002; 2002WO-US020993.

XX 06-JUL-2001; 2001US-0303634P.

XX (GETH) GENENTECH INC.

XX Held HA, Lasky LA, Laura RP, Sidhu SS, Wong WL, Wu Y;

XX WPI; 2003-267930/26.

XX New polypeptide that interacts with a 95 kDa post-synaptic density
 PT protein 95/Discs large/ZO-1 (PDZ) domain, useful for producing, selecting
 PT and identifying PDZ domain binding peptides.

XX Example 3; SEQ ID NO 185; 228pp; English.

XX The present invention describes an isolated polypeptide (I) that
 CC interacts with a 95 kDa post-synaptic density protein (PSD-95)/Discs
 CC large/ZO-1 (PDZ) domain. Also described: (1) a fusion protein (II)
 CC comprising a portion of a phage coat protein bonded through its carboxyl-
 CC terminus, optionally through a peptide linker, to a PDZ domain binding
 CC peptide, where the peptide contains 3-20 amino acid residues; (2) a
 CC library of (II), where the fusion proteins in the library comprise a
 CC number of PDZ domain binding peptides; (3) an assay for a PDZ domain
 CC binding compound; (4) a polypeptide that binds to the same epitope as
 CC (I), or that competes for binding to a PDZ domain with (I); (5) a
 CC polynucleotide (PN) encoding (I); (6) inhibiting a polypeptide-
 CC polynucleotide interaction, by contacting a mixture comprising a first and a
 CC second polypeptide with an inhibitor of interaction between a PDZ domain
 CC and its ligand, where the first polypeptide comprises the PDZ domain and
 CC the second polypeptide comprises the ligand; (7) screening for a
 CC substance that modulates interaction between a PDZ domain polypeptide and
 CC a molecule known to bind to the PDZ domain of the polypeptide; and (8)
 CC screening (M) for a substance that inhibits binding of a PDZ domain
 CC polypeptide to a molecule known to bind to the PDZ domain of the
 CC polypeptide. (I) has cytostatic, neurotropic, neuroprotective,
 CC antiparkinsonian, neuroleptic, antitumor, immunosuppressive, pulmonary
 CC and muscular activities, and can be used in gene therapy. The library of
 CC a fusion protein (II) is useful for producing a PDZ domain binding
 CC peptide library, and for selecting PDZ domain binding peptides in
 CC recombinant host cells. The library of (II) is also useful for
 CC identifying a PDZ domain binding protein, by selecting PDZ domain binding
 CC peptides using a new method. PN is useful for gene therapy, and in
 CC diagnoses of diseases. (I) and PN are useful for treating a subject at
 CC risk of a disorder or having a disorder associated with aberrant PDZP,
 CC PDZD, PDZ interacting protein (PIP) or PDZ domain binding peptides (PDBP)
 CC expression or activity such as rickettsial diseases, murine typhus,
 CC chronic myeloid leukaemia, Alzheimer's disease, neurological disorders
 CC such as Parkinson's disease and schizophrenia, X-linked autoimmune
 CC enteropathy, tsutsugamushi disease, facioscapulohumeral muscular
 CC dystrophy, late onset demyelinating disease, Usher syndrome type 1
 CC (USH1), nitric oxide-mediated tissue damage, tumours and cystic fibrosis.
 CC (I) is useful to identify cognate protein ligands for the PDZ domains.
 CC Structural analysis of the peptides are useful to understand PDZ domain
 CC structure and function, and also to identify intracellular biological
 CC functions for these motifs and the proteins that contain them. The
 CC peptides are further useful as PDZ domain inhibitors and are also useful
 CC as structural models in the design of small molecule inhibitors/agonists
 CC of the binding interaction between a PDZ domain containing protein and
 CC its cognate ligand. The present sequence represents a peptide which is
 CC used in the exemplification of the present invention.

XX SQ Sequence 7 AA;

Query Match 59.1%; Score 26; DB 7; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGVFW 6
 ||||
 Db 1 GGGCSW 6

RESULT 8
 AAW58581
 ID AAW58581 standard; peptide; 5 AA.

XX AC AAW58581;

XX DT 17-OCT-2003 (revised)

XX DT 07-SEP-1998 (first entry)

XX DE Kojibiose phosphorylase peptide 357-361.

XX Kojibiose phosphorylase; Thermoanaerobium brockii; TKP1; hydrolyse;
 KW saccharide; beta-D-glucose-1-phosphoric acid; sweetener; stabiliser;
 KW pharmaceutical; food; cosmetic; thermostable.

OS Thermoanaerobacter brockii.

XX PN EP841398-A2.

XX PD 13-MAY-1998.

XX PF 07-NOV-1997; 97BP-00308981.

XX PF 08-NOV-1996; 96JP-00311235.

XX PR 03-MAR-1997; 97JP-00061710.

XX PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX PI Nishimoto T, Kubota M, Chaen H, Miyake T;

XX DR WPI; 1998-252942/23.

XX PT New kojibiose phosphorylase, especially from Thermoanaerobium - used to
 PT produce saccharide compositions, used as e.g. sweeteners or stabilisers
 PT in pharmaceuticals, foods and cosmetics.

XX PS Claim 4; Page 33; 42pp; English.

XX CC The present sequence represents a kojibiose phosphorylase peptide from
 CC Thermoanaerobium brockii. Kojibiose phosphorylase hydrolyses kojibiose in
 CC the presence of inorganic phosphate (Pi) and/or its salt to form D-
 CC glucose and beta-D-glucose-1-phosphoric acid and/or its salt. Saccharide
 CC compositions, containing a D-glucosyl-transferred saccharide, are used in
 CC e.g., foods, animal feeds, beverages, cosmetics, pharmaceuticals or
 CC tobacco as sweeteners, taste improvers, osmosis regulators, glossing
 CC agents, crystallisation inhibitors, anti-carriers agents, growth promoters
 CC for bifid bacteria and promoters of mineral absorption. They may also be
 CC used to stabilise pharmaceuticals e.g. cytokines, hormones, vaccines,
 CC antibiotics, enzymes and microorganisms. Kojibiose phosphorylase is used
 CC to produce kojibiose by contacting, in the presence of Pi, with maltose
 CC and maltose phosphorylase (MP) on maltose or trehalose phosphorylase (TP)
 CC on trehalose. The saccharide compositions have a sweetness which
 CC harmonises with substances which are sour, bitter, acidic, salty,
 CC astringent and delicious and is acid and heat tolerant. The high thermal
 CC stability of kojibiose phosphorylase makes possible large scale,
 CC relatively inexpensive production of D-glucosyl transferred saccharides
 CC which are normally difficult to produce. (Updated on 17-OCT-2003 to
 CC standardise OS field)

XX SQ Sequence 5 AA;

Query Match 56.8%; Score 25; DB 2; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6
 ||||
 Db 1 GHVFW 5

RESULT 9

AAW39859
 ID AAW39859 standard; peptide; 7 AA.

XX AC AAW39859;

XX DT 16-JUN-1998 (first entry)

XX DE Heavy chain CDR3 of catalytic antibody 19G8.

XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

XX OS Mus sp.

XX PN WO9749800-A1.

```

XX PD 31-DEC-1997.
XX PF
XX PR 25-JUN-1997; 97WO-US010965.
XX PR 25-JUN-1996; 96US-00672345.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Landry DW;
XX DR WPI; 1998-077166/07.
XX PT New catalytic antibodies able to decompose cocaine, single-chain
XX PT analogues - used to treat cocaine overdose and addiction, required in far
XX PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX PS Claim 4; Page 92; 147pp; English.
XX XX
XX CC AAW39857-59 represent the sequences of the heavy chain complementarity
XX CC determining regions (CDRs) of the catalytic antibody 19G8, which is able
XX CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
XX CC were prepared and used to immunise mice for production of hybridomas.
XX CC Catalytic antibodies were identified by their capacity to release 3H-
XX CC benzoic acid from 3H-phenyl cocaine. The 19G8 antibody was identified
XX CC using TSA1, which is an immunogenic conjugate of a phosphate monoester
XX CC transition state analogue. Antibody 19G8 has a per minute Kcat of 0.091.
XX CC The antibodies reduce the concentration of cocaine in a subject, and are
XX CC used particularly for the treatment of an overdose. They are also used
XX CC for treating addiction (by reducing the in vivo concentration that can be
XX CC achieved)
XX SQ Sequence 7 AA;
Query Match 56.8%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVF 5
DB 1 GGGLF 5

RESULT 10
AAW39874
ID AAW39874 standard; peptide; 7 AA.
XX AC AAW39874;
XX DT 16-JUN-1998 (first entry)
XX DE Heavy chain CDR3 of a catalytic antibody capable of degrading cocaine.
XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
XX KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX KW overdose; addiction.
XX OS Mus sp.
XX PN WO9749800-A1.
XX PD 31-DEC-1997.
XX PF 25-JUN-1997; 97WO-US010965.
XX PR 25-JUN-1996; 96US-00672345.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Landry DW;
XX DR WPI; 1998-077166/07.
XX PT New catalytic antibodies able to decompose cocaine, single-chain
XX PT analogues - used to treat cocaine overdose and addiction, required in far
XX PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX PS Claim 4; Page 92; 147pp; English.
XX XX
XX CC AAW39857-59 represent the sequences of the heavy chain complementarity
XX CC determining regions (CDRs) of the catalytic antibody 19G8, which is able
XX CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
XX CC were prepared and used to immunise mice for production of hybridomas.
XX CC Catalytic antibodies were identified by their capacity to release 3H-
XX CC benzoic acid from 3H-phenyl cocaine. The 19G8 antibody was identified
XX CC using TSA1, which is an immunogenic conjugate of a phosphate monoester
XX CC transition state analogue. Antibody 19G8 has a per minute Kcat of 0.091.
XX CC The antibodies reduce the concentration of cocaine in a subject, and are
XX CC used particularly for the treatment of an overdose. They are also used
XX CC for treating addiction (by reducing the in vivo concentration that can be
XX CC achieved)
XX SQ Sequence 7 AA;
Query Match 56.8%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVF 5
DB 1 GGGLF 5

RESULT 11
AAW39862
ID AAW39862 standard; peptide; 7 AA.
XX AC AAW39862;
XX DT 16-JUN-1998 (first entry)
XX DE Heavy chain CDR3 of catalytic antibody 15A10.
XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
XX KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX KW overdose; addiction.
XX OS Mus sp.
XX PN WO9749800-A1.
XX PD 31-DEC-1997.
XX PF 25-JUN-1997; 97WO-US010965.
XX PR 25-JUN-1996; 96US-00672345.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Landry DW;
XX DR WPI; 1998-077166/07.
XX PT New catalytic antibodies able to decompose cocaine, single-chain
XX PT analogues - used to treat cocaine overdose and addiction, required in far
XX PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX PS Claim 2; Page 93; 147pp; English.
XX XX
XX CC AAW39860-62 represent the sequences of the heavy chain complementarity
XX CC determining regions (CDRs) of the catalytic antibody 15A10, which is able
XX CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)

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XX PI Landry DW;
XX DR WPI; 1998-077166/07.
XX PT New catalytic antibodies able to decompose cocaine, single-chain
XX PT analogues - used to treat cocaine overdose and addiction, required in far
XX PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX PS Claim 1; Page 5; 147pp; English.
XX XX
XX CC AAW39872-74 represent the sequences of the heavy chain complementarity
XX CC determining regions (CDRs) of a catalytic antibody which is capable of
XX CC degrading cocaine. A series of cocaine transition state analogues (TSAs)
XX CC were prepared and used to immunise mice for production of hybridomas.
XX CC Catalytic antibodies were identified by their capacity to release 3H-
XX CC benzoic acid from 3H-phenyl cocaine. These antibodies were found to have
XX CC CDRs of the present sequence. The antibodies reduce the concentration of
XX CC cocaine in a subject, and are used particularly for the treatment of an
XX CC overdose. They are also used for treating addiction (by reducing the in
XX CC vivo concentration that can be achieved)
XX SQ Sequence 7 AA;
Query Match 56.8%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVF 5
DB 1 GGGLF 5

RESULT 11
AAW39862
ID AAW39862 standard; peptide; 7 AA.
XX AC AAW39862;
XX DT 16-JUN-1998 (first entry)
XX DE Heavy chain CDR3 of catalytic antibody 15A10.
XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
XX KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX KW overdose; addiction.
XX OS Mus sp.
XX PN WO9749800-A1.
XX PD 31-DEC-1997.
XX PF 25-JUN-1997; 97WO-US010965.
XX PR 25-JUN-1996; 96US-00672345.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Landry DW;
XX DR WPI; 1998-077166/07.
XX PT New catalytic antibodies able to decompose cocaine, single-chain
XX PT analogues - used to treat cocaine overdose and addiction, required in far
XX PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX PS Claim 2; Page 93; 147pp; English.
XX XX
XX CC AAW39860-62 represent the sequences of the heavy chain complementarity
XX CC determining regions (CDRs) of the catalytic antibody 15A10, which is able
XX CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)

```

CC were prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 15A10 antibody was identified
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester
 CC transition state analogue. Antibody 15A10 has a per minute Kcat of 2.3.
 CC The antibodies reduce the concentration of cocaine in a subject, and are
 CC used particularly for the treatment of an overdose. They are also used
 CC for treating addiction (by reducing the in vivo concentration that can be
 CC achieved)
 CC
 XX

SQ Sequence 7 AA;

Query Match 56.8%; Score 25; DB 2; Length 7;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVF 5
 |||:
 Db 1 GGGLF 5

RESULT 12

AAW39856
 ID AAW39856 standard; peptide; 7 AA.

XX

AC AAW39856;

XX

DT 16-JUN-1998 (first entry)

XX

DE Heavy chain CDR3 of catalytic antibody 9A3.

XX

KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addition.

XX

OS Mus sp.

XX

PN WO9749800-A1.

XX

PD 31-DEC-1997.

XX

PF 25-JUN-1997; 97WO-US010965.

XX

PR 25-JUN-1996; 96US-00672345.

XX

XX (UYCO) UNIV COLUMBIA NEW YORK.

PA

PI Landry DW;

XX

XX WPI; 1998-077166/07.

DR

XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX

PS Claim 6; Page 91; 147pp; English.

XX

AAW39854-56 represent the sequences of the heavy chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 9A3, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
 CC were prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 9A3 antibody was identified
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester
 CC transition state analogue. Antibody 9A3 has a per minute Kcat of 0.015.
 CC The antibodies reduce the concentration of cocaine in a subject, and are
 CC used particularly for the treatment of an overdose. They are also used
 CC for treating addiction (by reducing the in vivo concentration that can be
 CC achieved)
 CC

SQ Sequence 7 AA;

RESULT 14

AAU81231

ID AAU81231 standard; peptide; 7 AA.

XX

Query Match 56.8%; Score 25; DB 2; Length 7;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVF 5
 |||:
 Db 1 GGGLF 5

RESULT 13

AAW40897

ID AAW40897 standard; peptide; 7 AA.

XX

AC AAW40897;

XX

DT 27-AUG-2003 (revised)

DT

09-JUN-1998 (first entry)

XX

DE Leader sequence 16, development of substances against Bunyaviridae.

XX

KW Virus inhibitory peptide; inhibition; ligand library;
 KW competitive affinity-elution; prophylactic substance;
 KW combinatorial therapy; pathogen diagnosis; leader molecule.

XX

OS Bunyaviridae.

XX

PN WO9745743-A1.

XX

PD 04-DEC-1997.

XX

PF 30-MAY-1997; 97WO-FI000339.

XX

PR 30-MAY-1996; 96FI-00002269.

XX

XX (UYHE-) UNIV HELSINKI LICENSING LTD.

PA

XX

PI Lankinen H, Heiskanen T, Vaheri A, Lundkvist A;

XX

DR WPI; 1998-032807/03.

XX

PT Selection of target pathogen inhibiting substances - useful for
 PT comparative drug design to provide therapeutically active, protective and
 PT prophylactic substances.

XX

PS Claim 14; Page 68; 81pp; English.

XX

CC This is a peptide which is useful as a leader molecule. It is used for
 CC the development of substances active against enveloped pathogens such as
 CC viruses from the family Bunyaviridae. Its selection involved the
 CC reaction of a ligand library with the bound target pathogen and the
 CC pathogen bound ligands are subjected to competitive affinity-elution with
 CC at least one neutralising substance. The method is useful for comparative
 CC drug design to provide therapeutically active, protective and/or
 CC prophylactic substances and developing combinatorial therapies as well as
 CC for pathogen diagnostics. The method also identifies "leader molecules",
 CC which not only have great affinity, but also mimic the functions of known
 CC neutralising substances. (Updated on 27-AUG-2003 to correct OS field.)
 CC

SQ Sequence 7 AA;

Query Match 56.8%; Score 25; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFQW 7
 |||:
 Db 3 IFWQ 6

AC AAU81231;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human trkC antibody heavy chain CDR1 of variable region #1.
 XX
 KW Human; mouse; anti-trkC agonist monoclonal antibody; trkC; antibody;
 KW trkA; trkB; cisplatin-induced neuropathy; pyridoxine-induced neuropathy;
 KW peripheral neuropathy; diabetic neuropathy; neurodegenerative disease;
 KW large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour;
 KW nerve cell injury; blood cell disorder; leukopaenia; eosinopaenia; wound;
 KW basopaenia; lymphopaenia; monocytopenia; neutropaenia; cancer; ulcer;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
 KW sickle cell disease; cardiac ischaemia; cerebrovascular disorder;
 KW cellular degeneration; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200198361-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 22-JUN-2001; 2001WO-US020153.
 XX
 PR 22-JUN-2000; 2000US-0213141P.
 PR 05-OCT-2000; 2000US-0238319P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Devaux B, Hongo JS, Presta LG, Shelton DL;
 XX
 DR WPI; 2002-130790/17.
 XX
 XX
 PT Novel anti-trkC agonist monoclonal antibody useful for treating
 PT neurodegenerative disease, shows no significant cross-reactivity with
 PT trkA/trkB, and recognizes epitope in domain 5 of trkC.
 XX
 PS Claim 12; Fig 11; 121pp; English.
 XX
 CC The invention relates to an anti-trkC agonist monoclonal antibody which
 CC shows no significant cross-reactivity with trkA or trkB, and recognizes
 CC an epitope in domain 5 of trkC. The antibodies of the invention are
 CC effective in the treatment of cisplatin- or pyridoxine-induced
 CC neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre
 CC sensory neuropathy, neurodegenerative disease including amyotrophic
 CC lateral sclerosis, nerve cell injuries, disorders of insufficient blood
 CC cells such as leukopaenia including eosinopaenia, basopaenia,
 CC lymphopaenia, monocytopenia, neutropaenia, Alzheimer's disease,
 CC Parkinson's disease, Huntington's disease and tumours. The sequences are
 CC also useful for inducing angiogenesis for treating wounds, ulcers and
 CC diabetic complications of sickle cell disease, for treating cardiac
 CC ischaemia and cerebrovascular disorders and in the diagnosis of diseases
 CC involving cellular degeneration. Sequences AAU81229-AAU81284 represent
 CC human and mouse anti-trkC agonist monoclonal antibodies and antibody
 CC fragments of the invention
 XX
 SQ Sequence 7 AA;

Query Match 56.8%; Score 25; DB 5; Length 7;
 Best Local Similarity 60.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6
 || : ||
 Db 2 GGYW 6

RESULT 15
 AAU86976
 ID AAU86976 standard; peptide; 5 AA.
 XX
 AC AAU86976;
 XX

DT 21-MAY-2002 (first entry)
 XX
 DE Estradiol mimotope peptide #24.
 XX
 KW Estradiol; mimotope; estrone-3-glucuronide; steroid detection;
 KW immunoassay; phage display; immunogen.
 XX
 OS Synthetic.
 XX
 PN WO200212270-A1.
 XX
 PD 14-FEB-2002.
 XX
 PF 26-JUL-2001; 2001WO-EP008705.
 XX
 PR 03-AUG-2000; 2000EP-00306613.
 XX
 PA (UNIL) UNILEVER PLC.
 XX
 PA (UNIL) UNILEVER NV.
 XX
 PA (UNIL) HINDUSTAN LEVER LTD.
 XX
 PI Badley RA, Berry MJ, Williams SC;
 XX
 DR WPI; 2002-241729/29.
 XX
 XX
 PT Peptide mimotope capable of binding specifically to antibody specific to
 PT estradiol, useful for assaying presence and/or amount of estradiol,
 PT especially estrone-3-glucuronide in sample.
 XX
 PS Claim 3; Page 22; 57pp; English.
 XX
 CC The invention relates to a purified peptide mimotope capable of binding
 CC specifically to an antibody specific to estradiol. Also included are a
 CC solid support having immobilised (releasably or non-releasably) peptide
 CC mimotopes, an immunoassay test device for the detection of estradiol in
 CC the sample, comprising the mimotopes and an antibody capable of binding
 CC specifically to the mimotopes to generate a detectable signal and an
 CC isolated nucleic acid encoding the peptide mimotopes. The mimotope is
 CC useful for assaying the presence and/or amount of estradiol preferably
 CC estrone-3-glucuronide in a sample which is urine or serum sample to be
 CC tested and is also utilised in an immunoassay test device, and further
 CC can be used as immunogens. The mimotope be used to construct new, or
 CC improve the performance of old, immunoassay test formats and devices.
 CC They can, for example, be utilised essentially to tune the signal in
 CC conventional displacement assays for the detection of estradiol. The
 CC mimotope can be bound directly to certain assay surfaces which are
 CC otherwise non-compatible with estradiol on such surfaces needing to be
 CC bound to the surface by complexing with another - often proteinaceous -
 CC molecule. The mimotope is capable of being bound to the antigen-binding
 CC site of an antibody in a selective fashion in the presence of excess
 CC quantities of other undesired materials, and tightly enough (i.e. with
 CC high enough affinity) that when used in an immunoassay, it provides a
 CC useful result). The present sequence is a peptide mimotopes of the
 CC invention
 XX
 SQ Sequence 5 AA;

Query Match 54.5%; Score 24; DB 5; Length 5;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GVPFW 6
 || : ||
 Db 1 GUPFW 4

Search completed: August 3, 2005, 12:03:06
 Job time : 100.333 secs

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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:26 ; Search time 25 Seconds
(without alignments)

20.902 Million cell updates/sec

Title: US-09-910-582B-2

Perfect score: 44

Sequence: 1 GGGVFWQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 61165

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*

4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*

5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	44	100.0	7	3	US-09-326-718-2	Sequence 2, Appli
2	27	61.4	7	3	US-09-258-754-300	Sequence 300, App
3	27	61.4	7	3	US-09-042-107-300	Sequence 300, App
4	27	61.4	7	4	US-09-722-250D-300	Sequence 300, App
5	27	61.4	7	4	US-09-676-475A-300	Sequence 300, App
6	25	56.8	5	2	US-08-966-388-3	Sequence 3, Appli
7	25	56.8	5	3	US-09-188-403-3	Sequence 3, Appli
8	25	56.8	5	3	US-09-188-404-3	Sequence 3, Appli
9	25	56.8	5	3	US-09-281-259-3	Sequence 3, Appli
10	25	56.8	7	2	US-08-672-345C-60	Sequence 60, Appli
11	25	56.8	7	2	US-08-672-345C-63	Sequence 60, Appli
12	25	56.8	7	2	US-08-672-345C-66	Sequence 66, Appli
13	25	56.8	7	2	US-08-672-345C-78	Sequence 78, Appli
14	25	56.8	7	3	US-09-214-095D-60	Sequence 60, Appli
15	25	56.8	7	3	US-09-214-095D-63	Sequence 63, Appli
16	25	56.8	7	3	US-09-214-095D-66	Sequence 66, Appli
17	25	56.8	7	3	US-09-214-095D-74	Sequence 74, Appli
18	24	54.5	7	4	US-09-731-242A-49	Sequence 49, Appli
19	23	52.3	7	4	US-09-388-788-2	Sequence 2, Appli
20	23	52.3	7	4	US-09-731-242A-53	Sequence 53, Appli
21	22	50.0	5	1	US-07-969-307A-6	Sequence 6, Appli
22	22	50.0	5	2	US-08-868-497-8	Sequence 8, Appli
23	22	50.0	5	3	US-08-860-808E-14	Sequence 14, Appli
24	22	50.0	5	3	US-08-860-808E-24	Sequence 24, Appli
25	22	50.0	5	3	US-09-362-230-8	Sequence 8, Appli
26	22	50.0	5	5	PCT-US94-07926-8	Sequence 8, Appli
27	22	50.0	6	1	US-08-375-911A-8	Sequence 8, Appli

28	50.0	6	3	US-08-860-808E-4	Sequence 4, Appli
29	50.0	6	3	US-08-860-808E-8	Sequence 8, Appli
30	50.0	6	3	US-08-860-808E-9	Sequence 9, Appli
31	50.0	6	4	US-08-940-136-272	Sequence 272, App
32	50.0	6	4	US-08-877-605-272	Sequence 272, App
33	50.0	6	4	US-08-877-605-314	Sequence 314, App
34	50.0	6	4	US-08-877-605-323	Sequence 323, App
35	50.0	6	4	US-08-877-605-331	Sequence 331, App
36	50.0	6	4	US-09-913-763-1	Sequence 1, Appli
37	50.0	7	3	US-09-258-754-384	Sequence 384, App
38	50.0	7	3	US-09-042-107-384	Sequence 384, App
39	50.0	7	4	US-08-877-605-337	Sequence 337, App
40	50.0	7	4	US-09-722-250D-384	Sequence 384, App
41	50.0	7	4	US-09-676-475A-384	Sequence 384, App
42	47.7	6	1	US-07-596-867C-9	Sequence 9, Appli
43	47.7	6	1	US-08-167-939A-9	Sequence 9, Appli
44	47.7	6	1	US-08-567-538-9	Sequence 9, Appli
45	47.7	6	2	US-08-482-228-8	Sequence 8, Appli
46	47.7	6	3	US-08-482-528-8	Sequence 8, Appli
47	47.7	6	4	US-09-461-325-278	Sequence 278, App
48	47.7	6	4	US-09-302-357-65	Sequence 65, Appli
49	47.7	6	4	US-08-877-605-291	Sequence 291, App
50	47.7	6	4	US-10-012-542-278	Sequence 278, App
51	47.7	6	4	PCT-US91-07715A-9	Sequence 9, Appli
52	47.7	7	1	US-07-969-307A-14	Sequence 14, Appli
53	47.7	7	1	US-08-192-300-10	Sequence 10, Appli
54	47.7	7	1	US-08-877-605-273	Sequence 273, App
55	45.5	6	1	US-07-973-235A-12	Sequence 12, Appli
56	45.5	6	1	US-07-973-235A-13	Sequence 13, Appli
57	45.5	6	1	US-07-973-235A-24	Sequence 24, Appli
58	45.5	6	2	US-08-462-720-12	Sequence 12, Appli
59	45.5	6	2	US-08-462-720-13	Sequence 13, Appli
60	45.5	6	2	US-08-462-720-24	Sequence 24, Appli
61	45.5	7	1	US-07-956-700B-71	Sequence 71, Appli
62	45.5	7	1	US-08-476-537-71	Sequence 71, Appli
63	45.5	7	1	US-08-485-607-71	Sequence 71, Appli
64	45.5	7	2	US-08-475-879-71	Sequence 71, Appli
65	45.5	7	3	US-09-433-043B-71	Sequence 71, Appli
66	45.5	7	4	US-09-756-223A-10	Sequence 10, Appli
67	45.5	7	4	US-09-731-242A-48	Sequence 48, Appli
68	43.2	4	1	US-07-802-667-8	Sequence 8, Appli
69	43.2	4	1	US-07-802-667-11	Sequence 11, Appli
70	43.2	5	1	US-07-969-307A-7	Sequence 7, Appli
71	43.2	5	3	US-09-091-814-64	Sequence 64, Appli
72	43.2	5	3	US-09-376-463-12	Sequence 12, Appli
73	43.2	5	6	5217869-11	Patent No. 5217869
74	43.2	5	6	5217869-11	Patent No. 5217869
75	43.2	6	1	US-07-969-307A-12	Sequence 12, Appli
76	43.2	6	1	US-07-973-235A-18	Sequence 18, Appli
77	43.2	6	1	US-07-802-667-32	Sequence 32, Appli
78	43.2	6	1	US-08-375-911A-7	Sequence 7, Appli
79	43.2	6	2	US-08-462-720-18	Sequence 18, Appli
80	43.2	6	3	US-08-115-753-8	Sequence 8, Appli
81	43.2	6	3	US-08-635-928-2	Sequence 2, Appli
82	43.2	6	3	US-08-635-928-3	Sequence 3, Appli
83	43.2	7	1	US-07-968-781A-83	Sequence 83, Appli
84	43.2	7	1	US-07-969-307A-16	Sequence 16, Appli
85	43.2	7	1	US-08-062-024B-1	Sequence 1, Appli
86	43.2	7	1	US-08-325-562-3	Sequence 3, Appli
87	43.2	7	1	US-08-437-795-3	Sequence 3, Appli
88	43.2	7	2	US-08-540-406-13	Sequence 13, Appli
89	43.2	7	2	US-08-756-407-1	Sequence 1, Appli
90	43.2	7	2	US-08-637-759B-134	Sequence 134, App
91	43.2	7	2	US-08-871-355A-134	Sequence 134, App
92	43.2	7	3	US-08-656-055-13	Sequence 13, Appli
93	43.2	7	3	US-08-954-668-13	Sequence 13, Appli
94	43.2	7	3	US-09-201-945-134	Sequence 134, App
95	43.2	7	4	US-08-918-658-13	Sequence 13, Appli
96	43.2	7	4	US-09-724-631-13	Sequence 13, Appli
97	43.2	7	4	US-08-877-605-266	Sequence 266, App
98	43.2	7	4	US-08-954-701A-13	Sequence 13, Appli
99	43.2	7	4	US-09-192-854-5	Sequence 5, Appli
100	43.2	7	4		

ALIGNMENTS

RESULT 1
US-09-326-718-2
; Sequence 2, Application US/09326718
; Patent No. 6303573
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Mackenna, Deirdre A.
; TITLE OF INVENTION: Heart Homing Peptides and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-LJ 3512
; CURRENT APPLICATION NUMBER: US/09/326,718
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-326-718-2

Query Match 100.0%; Score 44; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7
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Db 1 GGGVFWQ 7

RESULT 2
US-09-258-754-300
; Sequence 300, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: US/09/258,754
; EARLIER FILING DATE: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 300
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-300

Query Match 61.4%; Score 27; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7
|||
Db 1 GGDVWNR 7

RESULT 3
US-09-042-107-300
; Sequence 300, Application US/09042107

; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 300
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-300

Query Match 61.4%; Score 27; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7
|||
Db 1 GGDVWNR 7

RESULT 4
US-09-722-250D-300
; Sequence 300, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 300
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-300

Query Match 61.4%; Score 27; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7
|||
Db 1 GGDVWNR 7

RESULT 5
US-09-676-475A-300
; Sequence 300, Application US/09676475A
; Patent No. 6784153
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LA 4377
; CURRENT APPLICATION NUMBER: US/09/676,475A

;; CURRENT FILING DATE: 1998-03-13
;; PRIOR APPLICATION NUMBER: 09/042,107
;; PRIOR FILING DATE: 1998-03-13
;; NUMBER OF SEQ ID NOS: 452
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 300
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-676-475A-300

Query Match 61.4%; Score 27; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7
|||
Db 1 GGDVWVR 7

RESULT 6
US-08-966-388-3
; Sequence 3, Application US/08966388
; Patent No. 5965412
; GENERAL INFORMATION:
; APPLICANT: Tomoyuki NISHIMOTO
; APPLICANT: Michio KUBOTA
; APPLICANT: Hiroto CHAEN
; APPLICANT: Toshio MIYAKE
; TITLE OF INVENTION: KOJIBIOSE-PHOSPHORYLASE, ITS PREPARATION AND USES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,388
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 311,235/1996
; FILING DATE: 8-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 61,710/97
; FILING DATE: 3-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal fragment
US-08-966-388-3

Query Match 56.8%; Score 25; DB 2; Length 5;

Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GGVFW 6
|||
Db 1 GHVFW 5

RESULT 7
US-09-188-403-3
; Sequence 3, Application US/09188403
; Patent No. 6066477
; GENERAL INFORMATION:
; APPLICANT: Tomoyuki NISHIMOTO
; APPLICANT: Michio KUBOTA
; APPLICANT: Hiroto CHAEN
; APPLICANT: Toshio MIYAKE
; TITLE OF INVENTION: KOJIBIOSE PHOSPHORYLASE, ITS PREPARATION AND USES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,403
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/966,388
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 61,710/97
; FILING DATE: 3-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal fragment
US-09-188-403-3

Query Match 56.8%; Score 25; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6
|||
Db 1 GHVFW 5

RESULT 8
US-09-188-404-3
; Sequence 3, Application US/09188404
; Patent No. 6140487
; GENERAL INFORMATION:
; APPLICANT: Tomoyuki NISHIMOTO

APPLICANT: Michio KUBOTA
APPLICANT: Hitoto CHAEN
APPLICANT: Toshio MIYAKE
TITLE OF INVENTION: KOJIBIOSE PHOSPHORYLASE, ITS PREPARATION AND USES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,404
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/966,388
FILING DATE:
FILING DATE: 3-MAR-1997
APPLICATION NUMBER: JP 61,710/97
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
US-09-188-404-3

Query Match 56.8%; Score 25; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6
Db 1 GHVFW 5

RESULT 9
US-09-281-259-3
Sequence 3, Application US/09281259
Patent No. 6204377
GENERAL INFORMATION:
APPLICANT: Tomoyuki NISHIMOTO
APPLICANT: Michio KUBOTA
APPLICANT: Hitoto CHAEN
APPLICANT: Toshio MIYAKE
TITLE OF INVENTION: KOJIBIOSE PHOSPHORYLASE, ITS PREPARATION AND USES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

APPLICANT: Michio KUBOTA
APPLICANT: Hitoto CHAEN
APPLICANT: Toshio MIYAKE
TITLE OF INVENTION: KOJIBIOSE PHOSPHORYLASE, ITS PREPARATION AND USES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/281,259
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/966,388
FILING DATE:
FILING DATE: 3-MAR-1997
APPLICATION NUMBER: JP 61,710/97
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
US-09-281-259-3

Query Match 56.8%; Score 25; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6
Db 1 GHVFW 5

RESULT 10
US-08-672-345C-60
Sequence 60, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids

;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-60

Query Match 56.8%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVF 5
|||:
Db 1 GGGLF 5

RESULT 11

US-08-672-345C-63
; Sequence 63, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-63

Query Match 56.8%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVF 5
|||:
Db 1 GGGLF 5

RESULT 12

US-08-672-345C-66
; Sequence 66, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:

;
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-66

Query Match 56.8%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVF 5
|||:
Db 1 GGGLF 5

RESULT 13

US-08-672-345C-78
; Sequence 78, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-78

Query Match 56.8%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGVF 5
| | | : |
Db 1 GGGLF 5

RESULT 14

US-09-214-095D-60
; Sequence 60, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 60
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-60

Query Match 56.8%; Score 25; DB 3; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGVF 5
| | | : |
Db 1 GGGLF 5

RESULT 15

US-09-214-095D-63
; Sequence 63, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 63
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-63

Query Match 56.8%; Score 25; DB 3; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGVF 5
| | | : |
Db 1 GGGLF 5

Search completed: August 3, 2005, 11:58:08
Job time : 26 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:57:01 ; Search time 89.3333 Seconds
(without alignments)
30.529 Million cell updates/sec

Title: US-09-910-582B-2

Perfect score: 44

Sequence: 1 GGGVFWQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 71902

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	7	9	US-09-782-650-1
2	44	100.0	7	10	US-09-910-582B-2
3	44	100.0	7	17	US-10-838-289-34
4	27	61.4	7	17	US-10-838-289-100
5	27	61.4	7	17	US-10-607-595-300
6	26	59.1	7	14	US-10-190-082-185
7	25	56.8	7	10	US-09-940-727B-60
8	25	56.8	7	10	US-09-940-727B-63
9	25	56.8	7	10	US-09-940-727B-66
10	25	56.8	7	10	US-09-940-727B-78
11	25	56.8	7	16	US-10-312-316-3
					Sequence 1, Appli
					Sequence 2, Appli
					Sequence 34, Appl
					Sequence 100, App
					Sequence 300, App
					Sequence 185, App
					Sequence 60, Appl
					Sequence 63, Appl
					Sequence 66, Appl
					Sequence 78, Appl
					Sequence 3, Appli

25	56.8	7	17	US-10-893-576-95	Sequence 95, Appl
25	56.8	7	17	US-10-893-576-98	Sequence 98, Appl
25	56.8	7	18	US-10-984-960A-22	Sequence 22, Appl
25	56.8	7	18	US-10-984-960A-77	Sequence 77, Appl
24	54.5	5	11	US-09-920-306-27	Sequence 27, Appl
24	54.5	6	14	US-10-285-045-30	Sequence 30, Appl
24	54.5	6	14	US-10-284-660-30	Sequence 30, Appl
24	54.5	6	15	US-10-306-631-70	Sequence 70, Appl
24	54.5	6	16	US-10-807-635-30	Sequence 30, Appl
24	54.5	6	17	US-10-936-138-30	Sequence 30, Appl
24	54.5	6	18	US-10-496-869-3	Sequence 3, Appli
24	54.5	7	9	US-09-731-242A-49	Sequence 49, Appl
24	54.5	7	18	US-10-783-786-49	Sequence 49, Appl
23	52.3	6	9	US-09-740-026A-28	Sequence 28, Appl
23	52.3	7	9	US-09-731-242A-53	Sequence 53, Appl
23	52.3	7	14	US-10-190-082-61	Sequence 61, Appl
23	52.3	7	14	US-10-277-217-7	Sequence 7, Appli
23	52.3	7	18	US-10-783-786-53	Sequence 53, Appl
22	50.0	5	15	US-10-359-363A-44	Sequence 44, Appl
22	50.0	5	15	US-10-359-363A-45	Sequence 45, Appl
22	50.0	5	18	US-10-887-775-21	Sequence 21, Appl
22	50.0	6	15	US-10-283-599-272	Sequence 272, App
22	50.0	6	15	US-10-359-363A-39	Sequence 39, Appl
22	50.0	6	15	US-10-359-363A-101	Sequence 101, App
22	50.0	6	16	US-10-848-750-1	Sequence 1, Appli
22	50.0	6	17	US-10-829-388-18	Sequence 18, Appl
22	50.0	6	17	US-10-735-916A-8	Sequence 8, Appli
22	50.0	6	18	US-10-887-775-20	Sequence 20, Appl
22	50.0	6	18	US-10-991-217-272	Sequence 272, App
22	50.0	7	14	US-10-220-033-21	Sequence 21, Appl
22	50.0	7	15	US-10-359-363A-38	Sequence 38, Appl
22	50.0	7	15	US-10-413-943-40	Sequence 40, Appl
22	50.0	7	17	US-10-607-595-384	Sequence 384, App
22	50.0	7	18	US-10-887-775-19	Sequence 19, Appl
21	47.7	4	9	US-09-211-691-18	Sequence 18, Appl
21	47.7	4	14	US-10-317-773-18	Sequence 18, Appl
21	47.7	4	14	US-10-317-428-18	Sequence 3, Appli
21	47.7	5	17	US-10-923-257-3	Sequence 3, Appli
21	47.7	5	17	US-10-923-257-5	Sequence 5, Appli
21	47.7	6	9	US-09-867-847-52	Sequence 52, Appl
21	47.7	6	14	US-10-012-542-278	Sequence 278, App
21	47.7	6	14	US-10-115-123-278	Sequence 278, App
21	47.7	6	14	US-10-190-082-667	Sequence 667, App
21	47.7	6	17	US-10-825-958-50	Sequence 50, Appl
21	47.7	6	18	US-10-808-834-278	Sequence 278, App
21	47.7	7	9	US-09-205-658-296	Sequence 296, App
21	47.7	7	9	US-09-828-708-20	Sequence 20, Appl
21	47.7	7	10	US-09-791-153A-20	Sequence 20, Appl
21	47.7	7	10	US-09-963-693-296	Sequence 296, App
21	47.7	7	17	US-10-630-009-20	Sequence 20, Appl
21	47.7	7	17	US-10-400-991-47	Sequence 47, Appl
20	45.5	5	15	US-10-400-991-47	Sequence 3, Appli
20	45.5	6	10	US-09-912-414-3	Sequence 41, Appl
20	45.5	6	10	US-09-800-187-41	Sequence 41, Appl
20	45.5	6	15	US-10-414-524-68	Sequence 68, Appl
20	45.5	6	17	US-10-808-187-1752	Sequence 1752, Ap
20	45.5	6	17	US-10-658-232-18	Sequence 18, Appl
20	45.5	7	9	US-09-731-242A-48	Sequence 48, Appl
20	45.5	7	10	US-09-372-656-41	Sequence 41, Appl
20	45.5	7	14	US-10-015-979-79	Sequence 79, Appl
20	45.5	7	14	US-10-190-082-11	Sequence 11, Appl
20	45.5	7	14	US-10-190-082-430	Sequence 430, App
20	45.5	7	14	US-10-293-371-26	Sequence 26, Appl
20	45.5	7	14	US-10-321-648-10	Sequence 10, Appl
20	45.5	7	15	US-10-367-580-196	Sequence 196, App
20	45.5	7	15	US-10-367-593-196	Sequence 196, App
20	45.5	7	15	US-10-367-594-196	Sequence 196, App
20	45.5	7	15	US-10-367-654-196	Sequence 196, App
20	45.5	7	15	US-10-367-658-196	Sequence 196, App
20	45.5	7	15	US-10-367-668-196	Sequence 196, App
20	45.5	7	16	US-10-367-674-196	Sequence 196, App
20	45.5	7	16	US-10-727-335-38	Sequence 38, Appl
20	45.5	7	17	US-10-759-731A-128	Sequence 128, App
20	45.5	7	17	US-10-939-309-137	Sequence 137, App

85 20 45.5 7 18 US-10-783-786-48 Sequence 48, Appl
86 20 45.5 7 19 US-11-014-403-1 Sequence 1, Appl
87 19 43.2 4 16 US-10-401-131-1 Sequence 1, Appl
88 19 43.2 5 10 US-09-972-656-34 Sequence 34, Appl
89 19 43.2 5 10 US-09-972-656-36 Sequence 36, Appl
90 19 43.2 5 10 US-09-972-656-40 Sequence 40, Appl
91 19 43.2 5 14 US-10-190-082-240 Sequence 240, Appl
92 19 43.2 5 14 US-10-247-960-12 Sequence 12, Appl
93 19 43.2 5 15 US-10-338-366-26 Sequence 26, Appl
94 19 43.2 5 15 US-10-436-549-362 Sequence 362, Appl
95 19 43.2 5 15 US-10-243-613-82 Sequence 82, Appl
96 19 43.2 5 16 US-10-712-425-362 Sequence 362, Appl
97 19 43.2 5 16 US-10-401-131-2 Sequence 2, Appl
98 19 43.2 5 17 US-10-773-032-362 Sequence 362, Appl
99 19 43.2 5 17 US-10-923-257-1 Sequence 1, Appl
100 19 43.2 6 10 US-09-809-638-746 Sequence 746, Appl

ALIGNMENTS

RESULT 1
US-09-782-650-1
; Sequence 1, Application US/09782650
; Patent No. US20020019350A1
; GENERAL INFORMATION:
; APPLICANT: Levine, Arnold J.
; APPLICANT: Mitterer, Artur
; APPLICANT: Falkner, Falko-Guenter
; APPLICANT: Scheiflinger, Friedrich
; APPLICANT: Dörner, Friedrich
; APPLICANT: Edwards Lifesciences Corporation
; TITLE OF INVENTION: Targeted Angiogenesis
; FILE REFERENCE: 20553D-000611US
; CURRENT APPLICATION NUMBER: US/09/782,650
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: US 09/324,079
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 09/327,045
; PRIOR FILING DATE: 1999-06-07
; PRIOR APPLICATION NUMBER: PCT/US00/14988
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:targeting
; OTHER INFORMATION: molecule
US-09-782-650-1

Query Match 100.0%; Score 44; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7
| | | | |
Db 1 GGGVFWQ 7

RESULT 2
US-09-910-582B-2
; Sequence 2, Application US/09910582B
; Publication No. US20030045476A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Mackenna, Deirdre A.
; TITLE OF INVENTION: Heart Homing Conjugates
; FILE REFERENCE: P-LJ 4857
; CURRENT APPLICATION NUMBER: US/09/910,582B
; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 09/326,718
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-910-582B-2

Query Match 100.0%; Score 44; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7
| | | | |
Db 1 GGGVFWQ 7

RESULT 3
US-10-838-289-34
; Sequence 34, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jinming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; FILE REFERENCE: CWRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Heart homing peptide
US-10-838-289-34

Query Match 100.0%; Score 44; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7
| | | | |
Db 1 GGGVFWQ 7

RESULT 4
US-10-838-289-100
; Sequence 100, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jinming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; FILE REFERENCE: CWRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Ovary homing peptide
US-10-838-289-100

Query Match 61.4%; Score 27; DB 17; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7
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DB 1 GGDVWWR 7

RESULT 5
US-10-607-595-300
; Sequence 300, Application US/10607595
; Publication No. US20050074812A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/10/607,595
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/722,250
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 300
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-607-595-300

Query Match 61.4%; Score 27; DB 17; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7
|||
DB 1 GGDVWWR 7

RESULT 6
US-10-190-082-185
; Sequence 185, Application US/10190082
; Publication No. US20030148264A1
; GENERAL INFORMATION:
; APPLICANT: Laeky, Lawrence A.
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Held, Heike A.
; TITLE OF INVENTION: PHASE DISPLAYED PDZ DOMAIN LIGANDS
; FILE REFERENCE: P1905R1
; CURRENT APPLICATION NUMBER: US/10/190,082
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 185
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: Synthetic
US-10-190-082-185

Query Match 59.1%; Score 26; DB 14; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGVFW 6
|||
DB 1 GGGCSW 6

RESULT 7
US-09-940-727B-60
; Sequence 60, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-60

Query Match 56.8%; Score 25; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVF 5
|||
DB 1 GGGLF 5

RESULT 8
US-09-940-727B-63
; Sequence 63, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-63

Query Match 56.8%; Score 25; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVVF 5
|||:|
Db 1 GGGLF 5

RESULT 9
US-09-940-727B-66
; Sequence 66, Application US/09940727B
; Publication No. US20030077793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-66

Query Match 56.8%; Score 25; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVVF 5
|||:|
Db 1 GGGLF 5

RESULT 10
US-09-940-727B-78
; Sequence 78, Application US/09940727B
; Publication No. US20030077793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
; NAME/KEY: MISC FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: any amino acid
US-09-940-727B-78

Query Match 56.8%; Score 25; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVVF 5
|||:|
Db 1 GGGLF 5

RESULT 11
US-10-312-316-3
; Sequence 3, Application US/10312316
; Publication No. US20040137513A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Hongo, Jo-Anne S.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shelton, David L.
; TITLE OF INVENTION: AGONIST ANTI-TRK-C MONOCLONAL ANTIBODIES
; FILE REFERENCE: GENENT.0400PC
; CURRENT APPLICATION NUMBER: US/10/312,316
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/238,319
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-312-316-3

Query Match 56.8%; Score 25; DB 16; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVVF 6
|||:|
Db 2 GGYW 6

RESULT 12
US-10-893-576-95
; Sequence 95, Application US/10893576
; Publication No. US20050118643A1
; GENERAL INFORMATION:
; APPLICANT: BURGESS, TERESA L.
; APPLICANT: COXON, ANGELA
; APPLICANT: GREEN, LARRY L.
; APPLICANT: ZHANG, KE
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
; FILE REFERENCE: 06843.0051-00000
; CURRENT APPLICATION NUMBER: US/10/893,576
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/488,681
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 95
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy chain
; OTHER INFORMATION: variable region CDR peptide
US-10-893-576-95

Query Match 56.8%; Score 25; DB 17; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVVF 6
|||:|
Db 2 GGYW 6

RESULT 13
US-10-893-576-98
; Sequence 98, Application US/10893576

Publication No. US20050118643A1
; GENERAL INFORMATION:
; APPLICANT: BURGESS, TERESA L.
; APPLICANT: COXON, ANGELA
; APPLICANT: GREEN, LARRY L.
; APPLICANT: ZHANG, KE
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
; FILE REFERENCE: 06843.0051-00000
; CURRENT APPLICATION NUMBER: US/10/893,576
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/488,681
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 98
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy chain
; OTHER INFORMATION: variable region CDR peptide
US-10-893-576-98

Query Match 56.8%; Score 25; DB 17; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6
||:|
Db 2 GGYW 6

RESULT 14
US-10-984-960A-22
; Sequence 22, Application US/10984960A
; Publication No. US20050142137A1
; GENERAL INFORMATION:
; APPLICANT: Gallo, Michael
; APPLICANT: Chui, Daniel
; APPLICANT: Zhong, Haihong
; APPLICANT: Ara, Gulshan
; APPLICANT: Larocheille, William J.
; TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
; FILE REFERENCE: Cura 970
; CURRENT APPLICATION NUMBER: US/10/984,960A
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 60/518,275
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 22
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-984-960A-22

Query Match 56.8%; Score 25; DB 18; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6
||:|
Db 2 GGYW 6

RESULT 15
US-10-984-960A-77
; Sequence 77, Application US/10984960A
; Publication No. US20050142137A1
; GENERAL INFORMATION:
; APPLICANT: Gallo, Michael
; APPLICANT: Chui, Daniel
; APPLICANT: Zhong, Haihong

APPLICANT: Ara, Gulshan
; APPLICANT: Larocheille, William J.
; TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
; FILE REFERENCE: Cura 970
; CURRENT APPLICATION NUMBER: US/10/984,960A
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 60/518,275
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 77
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-984-960A-77

Query Match 56.8%; Score 25; DB 18; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6
||:|
Db 2 GGYW 6

Search completed: August 3, 2005, 12:13:59
Job time : 90.3333 secs

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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:26 ; Search time 19 Seconds
(without alignments)
35.448 Million cell updates/sec

Title: US-09-910-582B-3

Perfect score: 43

Sequence: 1 HGRVRPH 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	39.5	6	2 JN0861	peptidyl-dipeptida
2	16	37.2	7	2 I48105	dihydrofolate redu
3	15	34.9	5	2 JN0860	peptidyl-dipeptida
4	15	34.9	5	2 JN0862	peptidyl-dipeptida
5	14	32.6	3	3 A60898	burstin - chicken
6	14	32.6	5	2 I40702	primase - Citrobac
7	13	30.2	7	2 A15398	choline oxidase (E
8	12	27.9	5	2 S53595	hypothetical prote
9	12	27.9	7	2 S16364	opacity protein P.
10	12	27.9	7	2 S16365	opacity protein P.
11	12	27.9	7	2 E33932	Ig mu chain D regi
12	11	25.6	4	1 ECXAA	antho-RFamide neur
13	11	25.6	4	2 A25844	antho-RF amide neu
14	11	25.6	5	2 PT0553	T-cell receptor be
15	11	25.6	5	2 PT0608	T-cell receptor be
16	11	25.6	6	2 PQ0008	angiotensin-conver
17	11	25.6	6	2 A60494	antineoplastic gly
18	11	25.6	6	2 I51434	H4 histone - Afric
19	11	25.6	6	2 B33922	Ig mu chain D regi
20	11	25.6	7	2 PT0667	T-cell receptor be
21	11	25.6	7	2 PT0655	T-cell receptor be
22	11	25.6	7	2 A58718	carnocin U149 - Ca
23	10	23.3	4	2 S17255	ribosomal protein
24	10	23.3	6	2 A20186	fatty-acid synthas
25	10	23.3	7	2 A28709	phosphonoacetaldeh
26	10	23.3	7	2 A26200	aggrecaen - Bovine
27	9	20.9	3	3 PQ0010	angiotensin-conver
28	9	20.9	4	2 A02147	phagocytosis-stimu
29	9	20.9	4	2 T30569	hypothetical prote

30	9	20.9	5	1	HOROHA	proctolin - Americ
31	9	20.9	5	2	C41225	copper resistance
32	9	20.9	5	2	A60411	proctolin - Atlant
33	9	20.9	6	2	S11024	hydrogensulfite re
34	9	20.9	6	2	A61140	sperm acrosomal pr
35	9	20.9	6	2	I37027	protamine Pl - gor
36	9	20.9	6	2	S78764	ribosomal protein
37	9	20.9	6	2	B26206	alpha-1,4-glucan-p
38	9	20.9	6	2	PT0568	T-cell receptor be
39	9	20.9	7	2	A60224	Met-enkephalin-Arg
40	9	20.9	7	2	A44428	platelet aggregati
41	9	20.9	7	2	A44818	vicilin 72K chain
42	9	20.9	7	2	A33098	244K exoantigen -
43	9	20.9	7	2	PT0520	T-cell receptor be
44	9	20.9	7	2	PT0620	T-cell receptor be
45	9	20.9	7	2	A39690	neural cell adhesi
46	9	20.9	7	2	PQ0777	NADH2 dehydrogenas
47	9	20.9	7	2	A61081	tryptophyllin, bas
48	8	18.6	3	3	RHSHT	thyroliiberin - she
49	8	18.6	3	3	A92971	thyroliiberin - eas
50	8	18.6	3	3	RHTDIO	thyroliiberin - Bom
51	8	18.6	3	3	GKHU	growth-modulating
52	8	18.6	3	3	RHPGT	thyroliiberin - pig
53	8	18.6	4	2	A48360	gamma subunit of P
54	8	18.6	4	2	I38888	COI intron 16 prot
55	8	18.6	4	2	S39390	myosin-light-chain
56	8	18.6	4	2	PL0140	carbon-monoxide de
57	8	18.6	4	2	PT0271	Ig heavy chain CRD
58	8	18.6	4	2	PT0712	T-cell receptor be
59	8	18.6	5	2	S70154	URF2 protein - xan
60	8	18.6	5	2	T10954	hypothetical prote
61	8	18.6	5	2	PQ0689	photosystem I 10.4
62	8	18.6	5	2	B61445	Leu-enkephalin - b
63	8	18.6	5	2	A61445	Met-enkephalin - b
64	8	18.6	5	2	S62883	seminal plasma pro
65	8	18.6	5	2	PT0597	T-cell receptor be
66	8	18.6	5	2	PT0572	T-cell receptor be
67	8	18.6	5	2	I40698	biotin B - Citroba
68	8	18.6	5	2	S11075	alcohol dehydrogen
69	8	18.6	6	2	A35890	RNA-directed DNA p
70	8	18.6	6	2	A61419	sarcosine dehydrog
71	8	18.6	6	2	A44916	mosquitocidal toxi
72	8	18.6	6	2	S29637	Jacalin beta-II ch
73	8	18.6	6	2	B56979	collagen alpha 1(I
74	8	18.6	6	2	A46474	Fc epsilon RIIB -
75	8	18.6	6	2	PT0693	T-cell receptor be
76	8	18.6	6	2	S71349	beta-crystallin B2
77	8	18.6	7	1	NYPG7	hypochalamic hepta
78	8	18.6	7	2	A60139	fatty-acid synthas
79	8	18.6	7	2	S21230	dermorphin (Trp-4,
80	8	18.6	7	2	S19630	ribosomal protein -
81	8	18.6	7	2	PQ0663	membrane protein -
82	8	18.6	7	2	S42407	gramicidin S synth
83	8	18.6	7	2	PN0150	omega-gliadin 1,
84	8	18.6	7	2	S71129	ICL2 protein - Par
85	8	18.6	7	2	PC1316	large granule L3 c
86	8	18.6	7	2	I50210	gene c-rel protein
87	8	18.6	7	2	PT0246	Ig heavy chain CRD
88	8	18.6	7	2	PT0283	Ig heavy chain CRD
89	8	18.6	7	2	PT0676	T-cell receptor be
90	8	18.6	7	2	PX0008	glucuronosyltransf
91	8	18.6	7	2	S66442	glutathione S-tran
92	8	18.6	7	2	A38671	peptidylglycine mo
93	8	18.6	7	2	S58797	serine/threonine-s
94	8	18.6	7	2	S29735	polyphosphate-gluc
95	8	18.6	7	2	S09066	globulin IV alpha
96	8	18.6	7	2	I46868	alpha-myosin heavy
97	8	18.6	7	2	S08606	hypothetical prote
98	8	18.6	7	4	I56695	hypothetical L2 pr
99	8	18.6	7	4	S15597	orf 4 rara 5'-regi
100	7	16.3	3	3	A43391	TRH-like tripeptid

ALIGNMENTS

RESULT 1

JN0861
 peptidyl-di-peptidase A inhibitory peptide C111 - striped bonito
 C;Species: Sarda orientalis (striped bonito)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C;Accession: JN0861
 R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
 A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide
 A;Reference number: JN0859; MUID:94080036; PMID:7764272
 A;Accession: JN0861
 A;Molecule type: protein
 A;Residues: 1-6 <MAT>
 A;Experimental source: liver
 C;Comment: The carboxyl end is essential for the protein's expression of angiotensin I-converting enzyme
 C;Superfamily: bradykinin-potentiating peptide
 C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 39.5%; Score 17; DB 2; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VRPH 7
 ||||
 DB 2 VYPH 5

RESULT 2

I48105
 dihydrofolate reductase - Chinese hamster (fragment)
 C;Species: Cricetus griseus (Chinese hamster)
 C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
 C;Accession: I48105
 R;Azizkhan, J.C.; Vaughn, J.P.; Christy, R.J.; Hamlin, J.L.
 Biochemistry 25, 6228-6236, 1986
 A;Title: Nucleotide sequence and nuclease hypersensitivity of the Chinese hamster dihydrofolate reductase
 A;Reference number: I48105; MUID:97076541; PMID:3024702
 A;Accession: I48105
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-7 <RES>
 A;Cross-references: GB:M14771; NID:G191055; PIDN:AAA35975.1; PID:G191056

Query Match 37.2%; Score 16; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VRP 6
 ||||
 DB 2 VRP 4

RESULT 3

JN0860
 peptidyl-di-peptidase A inhibitory peptide C107 - striped bonito
 C;Species: Sarda orientalis (striped bonito)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C;Accession: JN0860
 R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
 A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide
 A;Reference number: JN0859; MUID:94080036; PMID:7764272
 A;Accession: JN0860
 A;Molecule type: protein
 A;Residues: 1-5 <MAT>
 A;Experimental source: intestine
 C;Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin I-converting enzyme
 C;Superfamily: bradykinin-potentiating peptide
 C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 32.6%; Score 14; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HG 2
 ||||
 DB 2 HG 3

RESULT 6

I40702
 primase - Citrobacter diversus (fragment)
 C;Species: Citrobacter diversus
 C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Aug-1996
 C;Accession: I40702
 R;Versalovic, J.; Lupski, J.R.
 Mol. Microbiol. 8, 343-355, 1993
 A;Title: Conservation and evolution of the rpsU-dnaG-rpoD macromolecular synthesis (MMS)
 A;Reference number: I40702; MUID:93302510; PMID:8316085
 A;Accession: I40702
 A;Status: preliminary; translated from GB/EMBL/DBJ

Query Match 34.9%; Score 15; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PH 7
 ||||
 DB 3 PH 4

RESULT 4

JN0862
 peptidyl-di-peptidase A inhibitory peptide C112 - striped bonito
 C;Species: Sarda orientalis (striped bonito)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C;Accession: JN0862
 R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
 A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide
 A;Reference number: JN0859; MUID:94080036; PMID:7764272
 A;Accession: JN0862
 A;Molecule type: protein
 A;Residues: 1-5 <MAT>
 A;Experimental source: intestine
 C;Comment: The amino terminal tripeptide of this protein inhibits angiotensin I-converting enzyme
 C;Superfamily: bradykinin-potentiating peptide
 C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 34.9%; Score 15; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VRP 6
 :|||
 DB 1 IRP 3

RESULT 5

A60898
 bursin - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
 C;Accession: A60898
 R;Audhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.
 Science 231, 997-999, 1986
 A;Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone of the bursin family
 A;Reference number: A60898; MUID:86122916; PMID:3484838
 A;Accession: A60898
 A;Molecule type: protein
 A;Residues: 1-3 <AUD>
 C;Keywords: amidated carboxyl end; hormone
 F;3/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 32.6%; Score 14; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HG 2
 ||||
 DB 2 HG 3

A;Molecule type: DNA
 A;Residues: 1-5 <RES>
 A;Cross-references: GB:L01754; NID:g144439
 C;Genetics:
 A;Gene: dnaG

Query Match 32.6%; Score 14; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GRV 4
 ||:
 Db 3 GRI 5

RESULT 7
 A15398
 choline oxidase (EC 1.1.3.17) - Alcaligenes sp. (tentative sequence) (fragment)
 C;Species: Alcaligenes sp.
 C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
 C;Accession: A15398
 R;Ohta-Fukuyama, M.; Miyake, Y.; Emi, S.; Yamano, T.
 J. Biochem. 88, 197-203, 1980
 A;Title: Identification and properties of the prosthetic group of choline oxidase from A
 A;Reference number: A15398; MUID:81006769; PMID:6997283
 A;Accession: A15398
 A;Molecule type: protein
 A;Residues: 1-7 <OHT>
 A;Cross-references: UNIPROT:P16101
 C;Keywords: oxidoreductase

Query Match 30.2%; Score 13; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HGR 3
 ||:
 Db 5 HSR 7

RESULT 8
 S53595
 hypothetical protein (upstream of transcription factor, CCAAT-binding) - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
 R;Calkhoven, C.F.; Bouwman, P.R.J.; Snippe, L.; Ab, G.
 Nucleic Acids Res. 22, 5540-5547, 1994
 A;Title: Translation start site multiplicity of the CCAAT/enhancer binding protein alpha
 A;Reference number: S53595; MUID:95140613; PMID:7838705
 A;Accession: S53595
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-5 <CAL>
 A;Cross-references: EMBL:X66844

Query Match 27.9%; Score 12; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GRV 4
 ||:
 Db 3 GRL 5

RESULT 9
 S16364
 opacity protein P.IIe - Neisseria gonorrhoeae (strain FA1090) (fragment)
 N;Alternate names: outer membrane protein P.IIe
 C;Species: Neisseria gonorrhoeae
 A;Variety: strain FA1090
 C;Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
 C;Accession: S16364

R;Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
 Infect. Immun. 55, 2026-2031, 1987
 A;Title: Antigenic and structural differences among six proteins II expressed by a single
 A;Reference number: S16360; MUID:87306843; PMID:3114142
 A;Accession: S16364
 A;Molecule type: protein
 A;Residues: 1-7 <BAR>
 A;Experimental source: strain FA1090
 A;Note: expression of opacity proteins is regulated by the number of translated repeat e)
 of repeats place the start codon in frame with the rest of the protein
 C;Superfamily: opacity protein
 C;Keywords: cell surface component; transmembrane protein
 F;1-7/Product: opacity protein P.IIe (fragment) #status experimental <MAT>

Query Match 27.9%; Score 12; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGR 3
 ||:
 Db 5 NGR 7
 RESULT 10
 S16365
 opacity protein P.IIf - Neisseria gonorrhoeae (strain FA1090) (fragment)
 N;Alternate names: outer membrane protein P.IIf
 C;Species: Neisseria gonorrhoeae
 A;Variety: strain FA1090
 C;Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
 C;Accession: S16365
 R;Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
 Infect. Immun. 55, 2026-2031, 1987
 A;Title: Antigenic and structural differences among six proteins II expressed by a single
 A;Reference number: S16360; MUID:87306843; PMID:3114142
 A;Accession: S16365
 A;Molecule type: protein
 A;Residues: 1-7 <BAR>
 A;Experimental source: strain FA1090
 A;Note: expression of opacity proteins is regulated by the number of translated repeat e)
 of repeats place the start codon in frame with the rest of the protein
 C;Superfamily: opacity protein
 C;Keywords: cell surface component; transmembrane protein
 F;1-7/Product: opacity protein P.IIf (fragment) #status experimental <MAT>

Query Match 27.9%; Score 12; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGR 3
 ||:
 Db 5 NGR 7
 RESULT 11
 E33932
 Ig mu chain D region (E7) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Aug-1996
 C;Accession: E33932
 R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
 Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
 A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-lin
 A;Reference number: A33932; MUID:89282823; PMID:2499887
 A;Accession: E33932
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-7 <BAC>
 A;Cross-references: GB:M27106
 C;Keywords: immunoglobulin

Query Match 27.9%; Score 12; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RP 6

Db 1 RP 2

RESULT 12

ECXXA

antho-RFamide neuropeptide - sea anemone (Anthopleura elegantissima)

C;Species: Anthopleura elegantissima

C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004

C;Accession: A26666

R;Grimmelikhuijzen, C.J.P.; Graff, D.

Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986

A;Title: Isolation of <Glu-Gly-Arg-Phe-NH₂ (Antho-RFamide), a neuropeptide from sea anemone

A;Reference number: A26666; MUID: 87092339; PMID: 2879288

A;Accession: A26666

A;Molecule type: protein

A;Residues: 1-4 <GRI>

A;Cross-references: UNIPROT:P10419

C;Comment: The function of this peptide is not known but it could act as a transmitter and

C;Superfamily: RFamide neuropeptide

C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match

Best Local Similarity 25.6%; Score 11; DB 1; Length 4;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GR 3

Db 2 GR 3

RESULT 13

A25844

autho-RF amide neuropeptide - sea pansy (Renilla koellikeri)

C;Species: Renilla koellikeri (Koelliker's sea pansy)

C;Date: 21-May-1988 #sequence_revision 30-Sep-1993 #text_change 11-Jul-1997

C;Accession: A25844

R;Grimmelikhuijzen, C.J.P.; Groeger, A.

FEBS Lett. 211, 105-108, 1987

A;Title: Isolation of the neuropeptide pGlu-Gly-Arg-Phe-amide from the pennatulid Renilla

A;Reference number: A25844

A;Accession: A25844

A;Molecule type: protein

A;Residues: 1-4 <GRI>

C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match

Best Local Similarity 25.6%; Score 11; DB 2; Length 4;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GR 3

Db 2 GR 3

RESULT 14

PT0553

T-cell receptor beta chain V-D-J region (126-1C) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0553

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID: 91277601; PMID: 1711558

A;Accession: PT0553

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FEE>

A;Experimental source: day 18 fetal thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match

Best Local Similarity 25.6%; Score 11; DB 2; Length 5;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GR 3

Db 3 GR 4

RESULT 15

PT0608

T-cell receptor beta chain V-D-J region (120-2CF) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004

C;Accession: PT0608

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID: 91277601; PMID: 1711558

A;Accession: PT0608

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FEE>

A;Cross-references: UNIPROT:O18345

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match

Best Local Similarity 25.6%; Score 11; DB 2; Length 5;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GR 3

Db 3 GR 4

Search completed: August 3, 2005, 11:42:32

Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:27 ; Search time 88.6667 Seconds
(without alignments)
40.427 Million cell updates/sec

Title: US-09-910-582B-3
Perfect score: 43
Sequence: 1 HGRVRPH 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 174

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	39.5	6	1	PVF1_PENNO
2	13	30.2	7	1	CHOX_ALCSP
3	12	27.9	7	2	O98866
4	12	27.9	7	2	P93233
5	11	25.6	5	1	E103_LITRU
6	11	25.6	5	1	UF01_MOUSE
7	11	25.6	7	1	LANC_CARUI
8	10	23.3	4	1	YIM1_YEAST
9	10	23.3	7	1	FAF2_ASCSU
10	10	23.3	7	1	FAF2_PANRE
11	10	23.3	7	1	FAF4_PANRE
12	10	23.3	7	2	Q8TAQ4
13	10	23.3	7	2	P82445
14	10	23.3	7	2	Q63480
15	9	20.9	4	1	TUFT_HUMAN
16	9	20.9	5	1	PRCT_CARMA
17	9	20.9	5	1	PRCT_LIMPO
18	9	20.9	5	1	PRCT_PERAM
19	9	20.9	6	1	QVM_LPDDE
20	9	20.9	6	1	VP19_HHV1K
21	9	20.9	7	1	ALL3_CARMA
22	9	20.9	7	1	ALL4_CARMA
23	9	20.9	7	1	ALL5_CARMA
24	9	20.9	7	1	GRFP_MOUSE
25	9	20.9	7	1	TPFY_PACDA
26	9	20.9	7	1	UF04_MOUSE
27	9	20.9	7	1	UN06_P1NPS
28	9	20.9	7	2	Q8NH77
29	9	20.9	7	2	O07354
30	8	18.6	3	1	GRMM_HUMAN
31	8	18.6	3	1	THYL_BOMOR

32	8	18.6	3	1	THYL_NOTVI	P62971 notophthalm
33	8	18.6	3	1	THYL_PIG	P62968 sus scrofa
34	8	18.6	3	1	THYL_SHEEP	P62969 ovis aries
35	8	18.6	4	1	DMCL_PSECH	P19916 pseudomonas
36	8	18.6	4	1	FVRI_ATEL	P58706 anthopleura
37	8	18.6	5	1	BIOB_CITFR	P12997 citrobacter
38	8	18.6	5	1	E104_LITRU	P82100 litoria rub
39	8	18.6	5	1	FARP_ARTTR	P41853 artiposthi
40	8	18.6	5	2	Q99007	Q99007 hordeum vul
41	8	18.6	6	1	SAPP_SEPOF	P83569 sepia offic
42	8	18.6	6	1	TMOF_SARBU	P41495 sarcophaga
43	8	18.6	6	1	TRPI_PSEPU	P36414 pseudomonas
44	8	18.6	7	1	FAFI_ASCSU	P31889 ascaris suu
45	8	18.6	7	1	FAR5_HIRME	P42564 hirudo medi
46	8	18.6	7	1	HV7_PIG	P01153 sus scrofa
47	8	18.6	7	1	TY51_LITRU	P82065 litoria rub
48	8	18.6	7	1	UF03_MOUSE	P38641 mus musculu
49	8	18.6	7	2	Q28742	Q28742 oryctolegus
50	8	18.6	7	2	Q99182	Q99182 gnatholebia
51	8	18.6	7	2	Q9C5B3	Q9C5B3 arabidopsis
52	8	18.6	7	2	P72081	P72081 nocardia la
53	8	18.6	7	2	Q47029	Q47029 enterobacte
54	8	18.6	7	2	Q8K3H6	Q8K3H6 rattus norv
55	8	18.6	7	2	Q65578	Q65578 bovine herp
56	8	18.6	7	2	Q66205	Q66205 transmissib
57	8	18.6	7	2	Q67113	Q67113 influenza a
58	7	16.3	4	2	Q16047	Q16047 homo sapien
59	7	16.3	5	1	BP77_BOTIN	P30425 bothrops in
60	7	16.3	5	1	FARP_CHICK	P83308 gallus gall
61	7	16.3	5	1	PAP2_PARMA	P81864 pardachirus
62	7	16.3	5	1	SUGA_ACHDO	P19991 acheta dome
63	7	16.3	6	1	CIP1_MYTED	P13736 mytilus edu
64	7	16.3	6	1	CIP2_MYTED	P13737 mytilus edu
65	7	16.3	6	1	E101_LITRU	P82096 litoria rub
66	7	16.3	6	2	P82181	P82181 spinacia ol
67	7	16.3	6	2	P82182	P82182 spinacia ol
68	7	16.3	7	1	ASCL_ALIAS	P84071 allium asca
69	7	16.3	7	1	BRHP_CONIM	P58803 conus imper
70	7	16.3	7	1	CARP_MYTED	P10420 mytilus edu
71	7	16.3	7	1	E105_LITRU	P82101 litoria rub
72	7	16.3	7	1	FARI_HELTI	P41871 helisma tr
73	7	16.3	7	1	FARB_CALVO	P41866 calliphora
74	7	16.3	7	1	ICAO_DACDE	P06294 dactylum d
75	7	16.3	7	1	MNPI_LEPDE	P83492 leptonotars
76	7	16.3	7	2	P83492	P83492 bionectria
77	7	16.3	7	2	P92210	P92210 agropyron c
78	7	16.3	7	2	P92214	P92214 amblyopyrum
79	7	16.3	7	2	P92218	P92218 australopyr
80	7	16.3	7	2	P92221	P92221 bromus iner
81	7	16.3	7	2	P92226	P92226 crithopsis
82	7	16.3	7	2	P92372	P92372 haynaldia v
83	7	16.3	7	2	P92381	P92381 hordeum bra
84	7	16.3	7	2	P92385	P92385 hordeum mar
85	7	16.3	7	2	P92387	P92387 henrardia p
86	7	16.3	7	2	P92390	P92390 heteranthe
87	7	16.3	7	2	P92393	P92393 hordeum vul
88	7	16.3	7	2	P92403	P92403 lophopyrum
89	7	16.3	7	2	P92421	P92421 peathyrosta
90	7	16.3	7	2	P92425	P92425 pseudoroegn
91	7	16.3	7	2	P92427	P92427 peridictyon
92	7	16.3	7	2	P92430	P92430 asgilops ta
93	7	16.3	7	2	P92440	P92440 thimopyrum
94	7	16.3	7	2	P92442	P92442 taeniathe
95	7	16.3	7	2	Q8MFY6	Q8MFY6 taraxacu
96	7	16.3	7	2	O50556	O50556 actinobacil
97	7	16.3	7	2	Q66113	Q66113 cherry leaf
98	7	16.3	7	2	Q9Y1Q9	Q9Y1Q9 human adeno
99	7	16.3	7	2	Q9Y1R0	Q9Y1R0 human adeno
100	7	16.3	7	2	Q9Y1E3	Q9Y1E3 human adeno

ALIGNMENTS

```

RESULT 1
PYFL_PENMO STANDARD; PRT; 6 AA.
AC P84005;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peptide tyrosine phenylalanine 1 (Pep-PYFL).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX PubMed=12431727; DOI=10.1016/S0196-9781(02)00176-6;
RA Sithigorngul P., Pupum J., Krungkasem C., Longyant S., Panchan N.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Four novel Pfys: members of NPY/PP peptide superfamily from the
RT eyestalk of the giant tiger prawn Penaeus monodon.";
RL Peptides 23:1895-1906(2002).
CC -1- FUNCTION: May act as a neurotransmitter, neuromodulator or
CC neuropeptide.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Limited to neuronal cell bodies, neuronal
CC processes and sinus gland.
CC -1- MASS SPECTROMETRY: MW=801.5; METHOD=MALDI; RANGE=1-6; NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the NPY family.
DR InterPro: IPR001955; Pancreatic hormn.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; PARTIAL.
DR PROSITE; PS00276; PANCREATIC_HORMONE_2; PARTIAL.
FW Amidation; Direct protein sequencing; Neuropeptide.
KT MOD RES 6 6 Phenylalanine amide (Potential).
SQ SEQUENCE 6 AA; 802 MW; 69D41774DCC46000 CRC64;

Query Match 39.5%; Score 17; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RVRP 6
DB 1 RARP 4

RESULT 2
CHOX_ALCSP STANDARD; PRT; 7 AA.
AC P16101;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Choline oxidase (EC 1.1.3.17) (Fragment).
OS Alcaligenes sp.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OX NCBI_TaxID=512;
RN [1]
RP SEQUENCE.
RX MEDLINE=81006769; PubMed=6997283;
RA Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
RT "Identification and properties of the prosthetic group of choline
RT oxidase from Alcaligenes sp.";
RL J. Biochem. 88:197-203(1980).
CC -1- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
DR PIR; A15398; A15398.
KW Direct protein sequencing; Oxidoreductase.
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match 30.2%; Score 13; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HGR 3
DB 5 HSR 7

RESULT 3
O98866 PRELIMINARY; PRT; 7 AA.
AC O98866;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome b/f subunit IV (Fragment).
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86120353; PubMed=3003688;
RA Sijben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.;
RT "Spinach plastid genes coding for initiation factor IF-1, ribosomal
RT protein S11 and RNA polymerase alpha-subunit.";
RL Nucleic Acids Res. 14:1029-1044(1986).
DR EMBL; X03496; CAA27215.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;

Query Match 27.9%; Score 12; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RP 6
DB 3 RP 4

RESULT 4
P93233 PRELIMINARY; PRT; 7 AA.
AC P93233;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
DE (Fragment).
GN Name=LE-ACS1B;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97351561; PubMed=9207843; DOI=10.1023/A:1005800511372;
RA Ostler J.H., Olson D.C., Shiu O.Y., Yang S.F.;
RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate
RT synthase genes by elicitor in suspension cultures of tomato
RT (Lycopersicon esculentum).";
RL Plant Mol. Biol. 34:275-286(1997).
DR EMBL; U75692; AAC49682.1; -.
DR GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Lyase.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;

```


Query Match 27.9%; Score 12; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RP 6
||
2 RP 3
DB

RESULT 5
ID E103 LITRU STANDARD; PRT; 5 AA.
AC P20209;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella".
RL Aust. J. Chem. 52:639-645 (1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD RES 5
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 25.6%; Score 11; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VRP 6
||
2 VHP 4
DB

RESULT 6
ID UF01 MOUSE STANDARD; PRT; 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=9500907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins using
RT preparative two-dimensional gel electrophoresis".
RL Electrophoresis 15:735-745 (1994).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.6, its MW is: 19 kDa.
KW Direct protein sequencing.
FT NON TER 5
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 25.6%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GR 3
||
3 GR 4
DB

RESULT 7
ID LANC CARUI STANDARD; PRT; 7 AA.
AC P36950;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lantibiotic carnocin UI49 (Fragment).
OS Carnobacterium sp. (strain UI49).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium
OX NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422 (1992).
CC -1- FUNCTION: Lantichione-containing peptide antibiotic (lantibiotic).
CC Active on Gram-positive bacteria.
KW Antibiotic; Bacteriocin; Direct protein sequencing; Lantibiotic.
FT NON TER 7
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 25.6%; Score 11; DB 1; Length 7;
Best Local Similarity 33.3%; Pred. No. 1.6e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 VRP 6
||
4 IQP 6
DB

RESULT 8
ID YLM1 YEAST STANDARD; PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (Yml1) (Fragment).
GN Names=YML1;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626; DOI=10.1016/0014-5793(91)80759-V;
RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria".
RL FEBS Lett. 284:51-56 (1991).
CC -1- FUNCTION: Putative component of the large subunit of mitochondrial
CC ribosome.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
DR PIR; S17255; S17255.
KW Direct protein sequencing; Mitochondrion; Ribosomal protein.
FT NON TER 4
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 23.3%; Score 10; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VRP 6
|
|
Db 2 VTP 4

RESULT 9
FAF2_ASCSU STANDARD; PRT; 7 AA.
AC P67879; P31890;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE FMRFamide-like neuropeptide AF2.
OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=93324431; PubMed=8332542; DOI=10.1016/0196-9781(93)90127-3;
RA Cowden C., Stretton A.O.W.;
RT "AF2, an Ascaris neuropeptide: Isolation, sequence, and bioactivity."
RL Peptides 14:423-430(1993).
CC -|- FUNCTION: Has effects on muscle tension.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Found in the nerve cords and a variety of ganglia particularly in the anterior regions.
CC -|- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 7 Phenylalanine amide.
SQ SEQUENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;

Query Match 23.3%; Score 10; DB 1; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HGRVR 5
|
|
Db 2 HEYLR 6

RESULT 10
FAF2_PANRE STANDARD; PRT; 7 AA.
AC P67880; P31890;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE FMRFamide-like neuropeptide AF2.
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE.
RX MEDLINE=95060998; PubMed=7970891;
RA Maule A.G., Shaw C., Bowman J.W.;
RT "The FMRFamide-like neuropeptide AF2 (Ascaris suum) is present in the free-living nematode, Panagrellus redivivus (Nematoda, Rhabditida)."
RL Parasitology 109:351-356(1994).
CC -|- FUNCTION: Has effects on muscle tension.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Found in the nerve cords and a variety of ganglia particularly in the anterior regions.
CC -|- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 7 Phenylalanine amide.
SQ SEQUENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;

Query Match 23.3%; Score 10; DB 1; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HGRVR 5
|
|
Db 2 HEYLR 6

Query Match 23.3%; Score 10; DB 1; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HGRVR 5
|
|
Db 2 HEYLR 6

RESULT 11
FAR4_PANRE STANDARD; PRT; 7 AA.
AC P41875;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRFamide-like neuropeptide PF4 (KPNFIRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95232026; PubMed=7716079; DOI=10.1016/0196-9781(94)00162-Y;
RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P., Thim L., Kubiak T.M., Martin R.A., Geary T.G.;
RT "Isolation and preliminary biological characterization of KPNFIRFamide, a novel FMRFamide-related peptide from the free-living nematode, Panagrellus redivivus."
RL Peptides 16:87-93(1995).
CC -|- FUNCTION: Myoactive; induces a rapid concentration-dependent muscle tension increase.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 7 Phenylalanine amide.
SQ SEQUENCE 7 AA; 921 MW; 69D40059C4576350 CRC64;

Query Match 23.3%; Score 10; DB 1; Length 7;
Best Local Similarity 33.3%; Pred. No. 1.6e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 RPH 7
|
|
Db 1 KPN 3

RESULT 12
Q8TAQ4 PRELIMINARY; PRT; 7 AA.
AC Q8TAQ4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE YAP1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.B., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2];
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC026212; AAH26212.2; -;
 SQ SEQUENCE 7 AA; 848 MW; 6AB2D1B6C2D406F0 CRC64;

Query Match 23.3%; Score 10; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RVR 5
 Db 2 RVQ 4

RESULT 13
 P82445 PRELIMINARY; PRT; 7 AA.
 AC P82445;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 10 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 CC lamids; Solanales; Solanaceae; Nicotiana.
 ON NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RL tobacco culture";
 RL Planta 0:0-0(2000).
 CC -!- SUBCELLULAR LOCATION: CELL WALL.
 CC -!- TISSUE SPECIFICITY: XYLEM.
 DR GO: 0005618; C:cell wall; IEA.
 KW Cell wall.
 FT NON TER 7
 SQ SEQUENCE 7 AA; 758 MW; 69D2C1E862D1B2A0 CRC64;

Query Match 23.3%; Score 10; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GRV 4
 Db 4 GHV 6

RESULT 14
 Q63480 PRELIMINARY; PRT; 7 AA.
 AC Q63480;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE TR4-NS orphan receptor (Fragment).

CN Name=TR4;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96198747; PubMed=8612486; DOI=10.1210/en.137.5.1562;
 RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
 RA Detera-Wadleigh S.D.;
 RT "Splice variants of rat TR4 orphan receptor: differential expression
 RT of novel sequences in the 5'-untranslated region and C-terminal
 RT domain";
 RL Endocrinology 137:1562-1571(1996).
 DR EMBL: U59125; AAB02827.1; -;
 DR GO: GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON TER 1
 SQ SEQUENCE 7 AA; 758 MW; 672AA87864005350 CRC64;

Query Match 23.3%; Score 10; DB 2; Length 7;
 Best Local Similarity 33.3%; Pred. No. 1.6e+06;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RVR 5
 Db 1 KIR 3

RESULT 15
 TUFT HUMAN STANDARD; PRT; 4 AA.
 AC P01858;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Phagocytosis-stimulating peptide (Tuftsin).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=72187087; PubMed=4112769;
 RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
 RT "The characteristics, isolation and synthesis of the phagocytosis
 RT stimulating peptide tuftsin";
 RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
 RN [2]
 RP IMMUNOGLOBULIN CLASS.
 RX MEDLINE=68091045; PubMed=4169272;
 RA Fidalgo B.V., Najjar V.A.;
 RT "The physiological role of the lymphoid system. VI. The stimulatory
 RT effect of leucophilic gamma globulin (leucokinin) on the phagocytic
 RT activity of human polymorphonuclear leucocyte.";
 RL Biochemistry 6:3386-3392(1967).
 CC -!- MISCELLANEOUS: An IGG (called leucokinin) binds reversibly to the
 CC cell membrane of neutrophils in the blood. Leucokininase on the
 CC membrane releases the active peptide tuftsin from the gamma chain.
 CC Tuftsin is essential for maximum stimulation of the phagocytic
 CC activity of neutrophils.
 DR PIR: A02147; A02147.
 DR MIM: 191150; -;
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006909; P:phagocytosis; NAS.
 KW Direct protein sequencing.
 SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

Query Match 20.9%; Score 9; DB 1; Length 4;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RP 6

Db :|
 2 KP 3

Search completed: August 3, 2005, 12:07:39
Job time : 90.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:27 ; Search time 96.3333 Seconds
(without alignments)
28.104 Million cell updates/sec

Title: US-09-910-582B-3

Perfect score: 43

Sequence: 1 HGRVRPH 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 121728

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	43	100.0	7	4	AAB30896 Peptide w
2	43	100.0	7	4	AAB50798 Heart hom
3	31	72.1	6	5	ABB77932 Amino aci
4	25	58.1	5	5	ABB77933 Amino aci
5	25	58.1	7	5	ABB77919 Amino aci
6	25	58.1	7	5	ABB77942 Amino aci
7	25	58.1	7	5	ABB77935 Amino aci
8	25	58.1	7	5	ABB77926 Amino aci
9	24	55.8	6	2	AAR83529 Zif268 zi
10	24	55.8	6	2	AAR84427 HIV-1 nuc
11	24	55.8	6	3	AAB14509 Sterile a
12	24	55.8	7	7	ABP98596 Clone #3
13	23	53.5	7	2	AAR74241 HJ loop p
14	22	51.2	6	2	AAR87203 Peptide d
15	22	51.2	6	2	AAR74242 HJ loop p
16	21	48.8	5	1	AAP90677 New anti
17	21	48.8	5	2	RAY34298 Consensus
18	21	48.8	6	2	AAR20413 Anti-b-en
19	21	48.8	7	7	ADC35979 Chemokine
20	20.5	47.7	7	5	ABG60380 Selective
21	20.5	47.7	7	6	ABR56826 Mouse adi
22	20.5	47.7	7	8	ADL95934 Adipose t
23	20	46.5	4	2	RAY13762 Human com
24	20	46.5	4	3	AAB14508 Sterile a
25	20	46.5	4	7	AAO29626 Anti-angi

26	46.5	4	7	ADD52664	Angiogene
27	46.5	4	8	ADK42403	Antibacte
28	46.5	4	8	ADK42404	Antibacte
29	46.5	5	2	AAR13624	Peptide f
30	46.5	5	7	ADD40737	Angiogene
31	46.5	6	2	AAR87734	Spacer #3
32	46.5	6	2	AAW87216	Peptide d
33	46.5	6	3	AAW96490	Factor VI
34	46.5	6	7	ADE10917	Chimeric
35	46.5	6	8	ADR12844	HBV surfa
36	46.5	7	2	AAR59473	Dynorphin
37	46.5	7	2	AAR59474	Dynorphin
38	46.5	7	2	AAR91327	Dynorphin
39	46.5	7	2	AAW45414	Hyaluroni
40	46.5	7	2	AAW60368	Tumour ho
41	46.5	7	2	AAV13795	Human fac
42	46.5	7	2	AAW93694	Human bre
43	46.5	7	2	AAV33954	Dynorphin
44	46.5	7	2	AAV33955	Dynorphin
45	46.5	7	2	AAV33960	Dynorphin
46	46.5	7	2	AAV33961	Dynorphin
47	46.5	7	3	AAB21785	Human bre
48	46.5	7	4	AAE06363	Human bre
49	46.5	7	4	ABP22401	HIV All m
50	46.5	7	5	ABG60853	Cellular
51	46.5	7	6	AAE31606	Soybean E
52	46.5	7	6	ABR57411	Brassica
53	46.5	7	6	ABR83390	Human int
54	46.5	7	6	ABU10392	Adeonarc
55	44.2	4	7	ADF55605	Peptide c
56	44.2	5	2	AAV23538	T-cell re
57	44.2	5	7	ADC13888	Rheumatoi
58	44.2	5	7	ADC13890	Rheumatoi
59	44.2	5	8	ADM09850	Human pro
60	44.2	5	8	ADR71016	Human pro
61	44.2	6	2	AAV20464	Human mic
62	44.2	6	2	AAW87134	Peptide d
63	44.2	6	2	AAW87136	Peptide d
64	44.2	6	2	AAW87133	Peptide d
65	44.2	6	2	AAW87135	Peptide d
66	44.2	6	2	AAW87131	Peptide d
67	44.2	6	2	AAW87132	Peptide d
68	44.2	6	2	AAV21747	Conserved
69	44.2	6	2	AAV05081	HIV Tat p
70	44.2	6	3	AAB39914	Anti-HIV1
71	44.2	6	4	AAB87889	Detector
72	44.2	6	4	AAG71004	Melanocor
73	44.2	6	4	AAE08962	Mammalian
74	44.2	6	4	AAB55481	Human ela
75	44.2	6	5	ABJ01251	Human cas
76	44.2	6	6	AAE32833	Human CEA
77	44.2	6	7	ABO32396	HIV-1 mul
78	44.2	6	7	ADE70909	HIV-1 Tat
79	44.2	6	7	ADL94402	HIV-1 Tat
80	44.2	6	8	ADK72016	Antimicro
81	44.2	6	8	ADO37518	Binding p
82	44.2	6	8	ADO28040	Capture s
83	44.2	6	8	ADR50217	6-mer pep
84	44.2	7	2	AAR09408	LFA-1 alp
85	44.2	7	2	AAW65198	Angiotens
86	44.2	7	2	AAW10759	Ferritin
87	44.2	7	2	AAW21064	Lipolytic
88	44.2	7	2	AAW23187	Terminal
89	44.2	7	2	AAW30417	HRE-I aff
90	44.2	7	2	AAW30387	HRE-I aff
91	44.2	7	2	AAW30443	HRE-I aff
92	44.2	7	2	AAV20236	Human mic
93	44.2	7	3	AAV84970	Amino aci
94	44.2	7	3	AAV84984	Amino aci
95	44.2	7	3	AAV67190	Cyskine
96	44.2	7	3	AAW23221	Hsp47-bln
97	44.2	7	3	AAV95630	Peptide u
98	44.2	7	7	ADC44279	Endotheli

99 19 44.2 7 7 ADC27877 Adc27877 Synthetic
100 19 44.2 7 7 AAO23601 Aao23601 Colon tum

ALIGNMENTS

RESULT 1
AAB30896
ID AAB30896 standard; peptide; 7 AA.
XX AC AAB30896;
XX DT 02-APR-2001 (first entry)
XX DE Peptide which selectively binds to normal cardiac endothelium.
XX KW Cardiac endothelium; angiogenic factor; vascular endothelium;
XX KW peripheral vascular disease; cardiovascular disease; angiogenesis;
XX KW cardiac neovascularisation.
XX OS Unidentified.
XX PN WO200075329-A1.
XX PD 14-DEC-2000.
XX PF 31-MAY-2000; 2000WO-US014988.
XX PR 07-JUN-1999; 99US-00327045.
XX PA (EDMA-) EDWARDS LIFESCIENCES CORP.
XX PA (BAXT) BAXTER AG.
XX PI Levine AJ, Mitterer A, Falkner F, Scheifflinger F, Dörner F;
XX DR WPI; 2001-091212/10.

XX New chimeric molecules having an angiogenic factor linked to a targeting
PT molecule that binds to a vascular endothelium, useful for increasing
PT cardiac neovascularization, or treating peripheral vascular and
PT cardiovascular diseases.

PS Disclosure; Page 27; 67pp; English.

XX AAB30895-99 represent targeting molecules, which are used to produce the
CC chimeric molecules of the invention. AAB30895-98 selectively bind to
CC normal cardiac endothelium. The specification describes a chimeric
CC molecule comprising an angiogenic factor linked to a targeting molecule
CC that specifically binds to a vascular endothelium. The chimeric molecules
CC are useful for treatment of peripheral vascular or cardiovascular
CC diseases. Specifically, they are useful for inducing or inhibiting
CC angiogenesis, for increasing cardiac neovascularisation in ischemic
CC tissue in the peripheral vascular system

XX Sequence 7 AA;

Query Match 100.0%; Score 43; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. NO. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGRVRPH 7
DB 1 HGRVRPH 7

RESULT 2
AAB50798
ID AAB50798 standard; peptide; 7 AA.
XX AC AAB50798;
XX DT 21-MAR-2001 (first entry)

XX Heart homing peptide SEQ ID NO: 3.
DE
XX Heart homing peptide; cardiovascular disease; ischaemic disease;
KW gene therapy.
XX OS Synthetic.
XX PN WO200075174-A1.
XX PD 14-DEC-2000.
XX PF 31-MAY-2000; 2000WO-US015088.
XX PR 07-JUN-1999; 99US-00326718.
XX PA (BURN-) BURNHAM INST.
XX PI Ruoslahti E, Mackenna DA;
XX DR WPI; 2001-071059/08.
XX Novel heart homing peptide that selectively homes to normal ischemic and
PT cardiac tissue useful for targeting ischemic tissues for treating
PT ischemic and cardiovascular diseases such as atherosclerosis and
PT restenosis.
XX Claim 2; Page 55; 70pp; English.

XX The present invention provides a number of heart homing peptides which
CC selectively home to cardiac tissue. These can be used in the treatment of
CC cardiovascular and ischaemic diseases, such as atherosclerosis, myocardial
CC thrombosis, restenosis, vasculitis, atherosclerotic aneurysms, myocardial
CC hypertrophy, congenital heart diseases, ischaemic heart disease and
CC anginas, acquired valvular/endocardial diseases, primary myocardial
CC diseases, cardiac tumours and arrhythmias

XX Sequence 7 AA;

Query Match 100.0%; Score 43; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. NO. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGRVRPH 7
DB 1 HGRVRPH 7

RESULT 3
AAB77932
ID ABB77932 standard; peptide; 6 AA.

XX ABB77932;
XX AC
XX DT 22-OCT-2002 (first entry)

DE Amino acid sequence of cyclopeptide P24 based on VEGF.

XX Cyclopeptide; vascular endothelial growth factor; VEGF; KDR receptor;
KW angiogenesis; tumour growth; metastasis development; ischaemia;
KW vascular eye disease; chronic inflammatory disease; tissue regeneration.

XX Synthetic.
XX PN FR2814744-A1.
XX PD 05-APR-2002.

XX PF 04-OCT-2000; 2000FR-00012654.
XX PR 04-OCT-2000; 2000FR-00012654.
XX PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.

PA (UYBO-) UNIV BORDEAUX 2 SEGALIN VICTOR.
 XX (UYBO-) UNIV BORDEAUX 1.
 PI Betz N, Bikfalvi A, Deleris G;
 XX WPI; 2002-502486/54.
 DR
 XX
 XX New cyclopeptides containing heptapeptide moiety acting as ligand for the
 PT KDR receptor of vascular endothelial growth factor (VEGF), useful,
 PT optionally in supported form, as angiogenesis inhibitors or activators.
 XX
 XX Disclosure; Page 45; 66pp; French.
 PS
 XX Claim 3; Page 45; 66pp; French.
 XX
 CC The present sequence represents a cyclopeptide, which contains a peptide
 CC (ABB77919) which is based on a partial sequence of vascular endothelial
 CC growth factor (VEGF). The arginine and glycine residues of ABB77919 are
 CC preferably linked by a chain of one or more compounds selected from
 CC natural or synthetic amino acids and organic compounds selected from
 CC group and an optionally substituted amino group. The cyclopeptides of the
 CC invention have high affinity for the KDR receptor of VEGF. The
 CC cyclopeptides mediate in angiogenesis by bonding to the KDR receptor of
 CC VEGF, and can be used to inhibit or promote angiogenesis. Inhibition of
 CC cyclopeptides mediate in angiogenesis by bonding to the KDR receptor of
 CC VEGF, and can be used to inhibit or promote angiogenesis. Inhibition of
 CC angiogenesis is potentially useful in combating tumour growth, metastasis
 CC development, ischaemia, vascular eye diseases and chronic inflammatory
 CC diseases; and promotion of angiogenesis is potentially useful in
 CC promoting tissue regeneration and colonization of implanted biomaterials
 CC such as bone substitutes
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 72.1%; Score 31; DB 5; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GRVRPH 7
 DB |||::|||
 1 GRIRPH 6
 RESULT 4
 ABB77913
 ID ABB77933 standard; peptide; 5 AA.
 XX
 AC ABB77933;
 XX
 DT 22-OCT-2002 (first entry)
 XX
 DE Amino acid sequence of VEGF-based peptide P1.
 XX
 KW Cyclopeptide; vascular endothelial growth factor; VEGF; KDR receptor;
 KW angiogenesis; tumour growth; metastasis development; ischaemia;
 KW vascular eye disease; chronic inflammatory disease; tissue regeneration.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "H attached"
 FT Modified-site 5
 FT /note= "OH attached"
 FT
 XX FR2814744-A1.
 XX
 XX 05-APR-2002.
 XX
 XX 04-OCT-2000; 2000FR-00012654.
 XX
 XX 04-OCT-2000; 2000FR-00012654.
 XX
 XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
 PA (UYBO-) UNIV BORDEAUX 2 SEGALIN VICTOR.
 PA (UYBO-) UNIV BORDEAUX 1.
 XX

PI Betz N, Bikfalvi A, Deleris G;
 XX WPI; 2002-502486/54.
 DR
 XX New cyclopeptides containing heptapeptide moiety acting as ligand for the
 PT KDR receptor of vascular endothelial growth factor (VEGF), useful,
 PT optionally in supported form, as angiogenesis inhibitors or activators.
 XX
 XX Disclosure; Page 42; 66pp; French.
 PS
 XX The specification describes cyclopeptides, which contain a peptide
 CC (ABB77919) which is based on a partial sequence of vascular endothelial
 CC growth factor (VEGF). The arginine and glycine residues of ABB77919 are
 CC preferably linked by a chain of one or more compounds selected from
 CC natural or synthetic amino acids and organic compounds have a carboxy
 CC group and an optionally substituted amino group. The cyclopeptides of the
 CC invention have high affinity for the KDR receptor of VEGF. The
 CC cyclopeptides mediate in angiogenesis by bonding to the KDR receptor of
 CC VEGF, and can be used to inhibit or promote angiogenesis. Inhibition of
 CC angiogenesis is potentially useful in combating tumour growth, metastasis
 CC development, ischaemia, vascular eye diseases and chronic inflammatory
 CC diseases; and promotion of angiogenesis is potentially useful in
 CC promoting tissue regeneration and colonization of implanted biomaterials
 CC such as bone substitutes. The present sequence represents a peptide,
 CC which is also base don VEGF
 XX
 XX Sequence 5 AA;
 SQ
 Query Match 58.1%; Score 25; DB 5; Length 5;
 Best Local Similarity 60.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 RVRPH 7
 DB |||::|||
 1 RIRPH 5
 RESULT 5
 ABB77919
 ID ABB77919 standard; peptide; 7 AA.
 XX
 AC ABB77919;
 XX
 DT 22-OCT-2002 (first entry)
 XX
 DE Amino acid sequence of a cyclopeptide based on VEGF.
 XX
 KW Cyclopeptide; vascular endothelial growth factor; VEGF; KDR receptor;
 KW angiogenesis; tumour growth; metastasis development; ischaemia;
 KW vascular eye disease; chronic inflammatory disease; tissue regeneration.
 XX
 OS Synthetic.
 XX
 PN FR2814744-A1.
 XX
 XX 05-APR-2002.
 XX
 XX 04-OCT-2000; 2000FR-00012654.
 XX
 XX 04-OCT-2000; 2000FR-00012654.
 XX
 XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
 PA (UYBO-) UNIV BORDEAUX 2 SEGALIN VICTOR.
 PA (UYBO-) UNIV BORDEAUX 1.
 XX
 XX Betz N, Bikfalvi A, Deleris G;
 XX WPI; 2002-502486/54.
 DR
 XX New cyclopeptides containing heptapeptide moiety acting as ligand for the
 PT KDR receptor of vascular endothelial growth factor (VEGF), useful,
 PT optionally in supported form, as angiogenesis inhibitors or activators.
 XX

PS Claim 1; Page 44; 66pp; French.

XX The present sequence represents a cyclopeptide, which is based on a

CC partial sequence of vascular endothelial growth factor (VEGF). The

CC arginine and glycine residues of the present peptide are preferably

CC linked by a chain of one or more compounds selected from natural or

CC synthetic aminoacids and organic compounds have a carboxy group and an

CC optionally substituted amino group. The cyclopeptides of the invention

CC have high affinity for the KDR receptor of VEGF. The cyclopeptides

CC mediate in angiogenesis by bonding to the KDR receptor of VEGF, and can

CC be used to inhibit or promote angiogenesis. Inhibition of angiogenesis is

CC potentially useful in combating tumour growth, metastasis development,

CC ischaemia, vascular eye diseases and chronic inflammatory diseases; and

CC promotion of angiogenesis is potentially useful in promoting tissue

CC regeneration and colonization of implanted biomaterials such as bone

CC substitutes

XX Sequence 7 AA;

SQ Query Match 58.1%; Score 25; DB 5; Length 7;

Best Local Similarity 60.0%; Pred. No. 1.8e+06;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVRPH 7

Db |::||

1 RIKPH 5

RESULT 6

ABB77942

ID ABB77942 standard; peptide; 7 AA.

XX AC ABB77942;

XX DT 22-OCT-2002 (first entry)

XX DE Amino acid sequence of VEGF-based peptide P18.

XX KW Cyclopeptide; vascular endothelial growth factor; VEGF; KDR receptor;

XX KW angiogenesis; tumour growth; metastasis development; ischaemia;

XX KW vascular eye disease; chronic inflammatory disease; tissue regeneration.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT FR2814744-A1.

PN 05-APR-2002.

PD 04-OCT-2000; 2000FR-00012654.

XX PF 04-OCT-2000; 2000FR-00012654.

XX PR 04-OCT-2000; 2000FR-00012654.

XX PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.

XX PA (UYBO-) UNIV BORDEAUX 2 SEGALLEN VICTOR.

XX PA (UYBO-) UNIV BORDEAUX 1.

XX PI Betz N, Bikfalvi A, Deleris G;

XX WPI; 2002-502486/54.

XX New cyclopeptides containing heptapeptide moiety acting as ligand for the

PT KDR receptor of vascular endothelial growth factor (VEGF), useful,

PT optionally in supported form, as angiogenesis inhibitors or activators.

PS Disclosure; Page 42; 66pp; French.

XX The specification describes cyclopeptides, which contain a peptide

CC growth factor (VEGF). The arginine and glycine residues of ABB77919 are

CC preferably linked by a chain of one or more compounds selected from

CC natural or synthetic amino acids and organic compounds have a carboxy

CC preferably linked by a chain of one or more compounds selected from

CC natural or synthetic amino acids and organic compounds have a carboxy

CC group and an optionally substituted amino group. The cyclopeptides of the

CC invention have high affinity for the KDR receptor of VEGF. The

CC cyclopeptides mediate in angiogenesis by bonding to the KDR receptor of

CC VEGF, and can be used to inhibit or promote angiogenesis. Inhibition of

CC angiogenesis is potentially useful in combating tumour growth, metastasis

CC development, ischaemia, vascular eye diseases and chronic inflammatory

CC diseases; and promotion of angiogenesis is potentially useful in

CC promoting tissue regeneration and colonization of implanted biomaterials

CC such as bone substitutes. The present sequence represents a peptide,

XX which is also base don VEGF

SQ Sequence 7 AA;

Query Match 58.1%; Score 25; DB 5; Length 7;

Best Local Similarity 60.0%; Pred. No. 1.8e+06;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVRPH 7

Db |::||

2 RIKPH 6

RESULT 7

ABB77935

ID ABB77935 standard; peptide; 7 AA.

XX AC ABB77935;

XX DT 22-OCT-2002 (first entry)

XX DE Amino acid sequence of VEGF-based peptide P3.

XX KW Cyclopeptide; vascular endothelial growth factor; VEGF; KDR receptor;

XX KW angiogenesis; tumour growth; metastasis development; ischaemia;

XX KW vascular eye disease; chronic inflammatory disease; tissue regeneration.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "H attached"

FT Modified-site 7 /note= "OH attached"

FT FR2814744-A1.

PN 05-APR-2002.

PD 04-OCT-2000; 2000FR-00012654.

XX PF 04-OCT-2000; 2000FR-00012654.

XX PR 04-OCT-2000; 2000FR-00012654.

XX PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.

XX PA (UYBO-) UNIV BORDEAUX 2 SEGALLEN VICTOR.

XX PA (UYBO-) UNIV BORDEAUX 1.

XX PI Betz N, Bikfalvi A, Deleris G;

XX WPI; 2002-502486/54.

XX New cyclopeptides containing heptapeptide moiety acting as ligand for the

PT KDR receptor of vascular endothelial growth factor (VEGF), useful,

PT optionally in supported form, as angiogenesis inhibitors or activators.

PS Disclosure; Page 42; 66pp; French.

XX The specification describes cyclopeptides, which contain a peptide

CC growth factor (VEGF). The arginine and glycine residues of ABB77919 are

CC preferably linked by a chain of one or more compounds selected from

CC natural or synthetic amino acids and organic compounds have a carboxy

CC group and an optionally substituted amino group. The cyclopeptides of the
 CC invention have high affinity for the KDR receptor of VEGF. The
 CC cyclopeptides mediate in angiogenesis by bonding to the KDR receptor of
 CC VEGF, and can be used to inhibit or promote angiogenesis. Inhibition of
 CC angiogenesis is potentially useful in combating tumour growth, metastasis
 CC development, ischaemia, vascular eye diseases and chronic inflammatory
 CC diseases; and promotion of angiogenesis is potentially useful in
 CC promoting tissue regeneration and colonization of implanted biomaterials
 CC such as bone substitutes. The present sequence represents a peptide,
 CC which is also base don VEGF

XX Sequence 7 AA;

Query Match 58.1%; Score 25; DB 5; Length 7;
 Best Local Similarity 60.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RVRPH 7
 |::||
 Db 1 RIKPH 5

RESULT 8

ABE77926
 ID ABE77926 standard; peptide; 7 AA.

XX AC ABE77926;

XX 22-OCT-2002 (first entry)

DE Amino acid sequence of cyclopeptide P16 based on VEGF.

XX Cyclopeptide; vascular endothelial growth factor; VEGF; KDR receptor;
 KW angiogenesis; tumour growth; metastasis development; ischaemia;
 KW vascular eye disease; chronic inflammatory disease; tissue regeneration.

OS Synthetic.

XX FR2814744-A1.

XX 05-APR-2002.

XX 04-OCT-2000; 2000FR-00012654.

XX 04-OCT-2000; 2000FR-00012654.

XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.

XX (UYBO-) UNIV BORDEAUX 2 SEGALLEN VICTOR.

XX (UYBO-) UNIV BORDEAUX 1.

XX Betz N, Bikkalvi A, Deleris G;

XX WPI; 2002-502486/54.

XX New cyclopeptides containing heptapeptide moiety acting as ligand for the
 PT KDR receptor of vascular endothelial growth factor (VEGF), useful,
 PT optionally in supported form, as angiogenesis inhibitors or activators.

XX Claim 3; Page 44; 66pp; French.

XX The present sequence represents a cyclopeptide, which contains a peptide
 CC (ABE77919) which is based on a partial sequence of vascular endothelial
 CC growth factor (VEGF). The arginine and glycine residues of ABE77919 are
 CC preferably linked by a chain of one or more compounds selected from
 CC natural or synthetic amino acids and organic compounds have a carboxy
 CC group and an optionally substituted amino group. The cyclopeptides of the
 CC invention have high affinity for the KDR receptor of VEGF. The
 CC cyclopeptides mediate in angiogenesis by bonding to the KDR receptor of
 CC VEGF, and can be used to inhibit or promote angiogenesis. Inhibition of
 CC angiogenesis is potentially useful in combating tumour growth, metastasis
 CC development, ischaemia, vascular eye diseases and chronic inflammatory
 CC diseases; and promotion of angiogenesis is potentially useful in
 CC promoting tissue regeneration and colonization of implanted biomaterials

CC such as bone substitutes
 XX Sequence 7 AA;

Query Match 58.1%; Score 25; DB 5; Length 7;
 Best Local Similarity 60.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RVRPH 7
 |::||
 Db 1 RIKPH 5

RESULT 9

AAR83529
 ID AAR83529 standard; protein; 6 AA.

XX AC AAR83529;

XX 23-APR-1996 (first entry)

DE Zif268 zinc finger 2 randomised residues with affinity for HIV-1.

XX zinc finger; variant; randomised; alpha-helical region; Zif268;
 KW customised affinity; cancer; therapy; virus infection; HIV-1;
 KW human immunodeficiency virus; consensus target sequence;
 KW transcription-activator; transcription-inhibitor; plant disease.

OS Synthetic.

XX WO9519431-A1.

XX 20-JUL-1995.

XX 18-JAN-1995; 95WO-US0000829.

XX 18-JAN-1994; 94US-00183119.

XX 28-SEP-1994; 94US-00312604.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Gottesfeld JM, Wright PE;

XX WPI; 1995-263862/34.

XX New zinc finger-nucleotide binding polypeptide(s) - used for modulating
 PT the function of cellular nucleotide sequences, partic. for treating cell
 PT proliferative disorders.

XX Example 10; Fig 9; 135pp; English.

XX Regions of the alpha-helix in each of the Zif268 zinc fingers 1, 2 and 3
 CC were randomised and selected for binding to particular conserved target
 CC sequences in HIV-1. In finger 2, the randomised residues were at
 CC positions -2,-1,1,2,3 and 4 in the alpha-helical region. The present
 CC sequence has affinity for the TGG target sequence. Zinc finger proteins
 CC are useful for suppressing transcription and therefore for treating
 CC proliferative disorders

XX Sequence 6 AA;

Query Match 55.8%; Score 24; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VRPH 7
 |::||
 Db 1 VRPH 4

RESULT 10

AAW84427
 ID AAW84427 standard; peptide; 6 AA.

XX AAW84427;
AC
XX
DT 22-MAR-1999 (first entry)
DE
XX HTV-1 nucleic acid binding protein zinc finger 2 peptide.
XX
KW zinc finger; nucleotide-binding protein; cell proliferative disorder;
KW gene therapy; cancer; psoriasis; pemphigus vulgaris; Bechet's syndrome;
KW lipid histiocytosis; human immune deficiency virus; HIV; viral infection;
KW transgenic plant.
XX
OS Synthetic.
XX
XX WO9854311-A1.
XX
XX 03-DEC-1998.
XX
XX 27-MAY-1998; 98WO-US010801.
XX
XX 27-MAY-1997; 97US-00863813.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Barbas CP, Gottesfeld JM, Wright PE;
PI
XX WPI; 1999-059831/05.
XX
XX New zinc finger nucleotide-binding protein variant that modulates
PT selected nucleotide sequence - used for treatment of proliferative and
PT viral diseases by gene therapy, and can be made selective for any target
PT sequence.
XX
XX Example 10; Fig 9; 158pp; English.
XX
CC AAW84422-41 represent the peptides obtained from randomised finger 2
CC sequences of zinc finger nucleotide-binding proteins that bind to HIV-1
CC target sequences. The peptides were produced in the course of the
CC invention. The specification describes zinc finger nucleotide-binding
CC protein variants with at least two zinc finger modules that bind to a
CC cellular nucleotide sequence and modulate its function. Zinc finger
CC proteins, and compositions containing them, are used to increase or
CC reduce transcription of a gene linked to the cellular nucleotide
CC sequence. The proteins are used specifically for treating or preventing
CC cell proliferative disorders (in humans, animals or plants, including
CC those induced by viruses), particularly where expressed from nucleic acid
CC by gene therapy (including ex vivo methods). Typical diseases that can be
CC treated are many forms of cancer, psoriasis, pemphigus vulgaris, Bechet's
CC syndrome and lipid histiocytosis, also treatment of human immune
CC deficiency virus (HIV) and other viral infections, and production of
CC transgenic plants resistant to bacterial and viral diseases. The present
CC oligonucleotide is used in the course of the invention
XX
SQ Sequence 6 AA;
Query Match 55.8%; Score 24; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 VRPH 7
| | | |
DB 1 VRPH 4
RESULT 11
AAB14509
ID AAB14509 standard; peptide; 6 AA.
AC AAB14509;
XX
XX 14-NOV-2000 (first entry)
DT
XX Sterile alpha motif (SAM) domain peptide, SEQ ID NO:110.

XX SAM domain; sterile alpha motif; homodimerisation; heterodimerisation;
KW signal transduction; X-ray crystallography; protein coordinate data;
KW drug development; antibody; T-cell signalling; telomere function;
KW cell proliferative disorder; senescence; ageing; cancer; atherosclerosis;
KW arthritis; angiogenesis; neuronal development; axonal migration;
KW neurodegeneration; neurodegenerative disease; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; demyelinating disease;
KW multiple sclerosis; amyotrophic lateral sclerosis; nervous system trauma;
KW stroke; ischaemia; cytostatic; immunosuppressive; vulnerability;
KW neuroprotective; neurotropic; antiparkinsonian; cerebroprotective;
KW antiarthritic; antiatherosclerotic.
XX
OS Unidentified.
XX
XX WO200037500-A1.
XX
XX 29-JUN-2000.
XX
XX 17-DEC-1999; 99WO-CA001209.
XX
XX 18-DEC-1998; 98US-0112929P.
XX
XX (MOUN) MOUNT SINAI HOSPITAL.
XX
XX Stapleton D, Sicheri F;
PI
XX WPI; 2000-442645/38.
DR
XX
XX 3-D structure of sterile alpha motif domain used as model for determining
PT 3-D structures of additional native or mutated SAM domain with unknown
PT structure and structures of co-crystals of SAM domain with modulators.
XX
XX Claim 24; Page 48; 72pp; English.
XX
CC The invention relates to the three dimensional structure of a SAM (sterile
CC alpha motif) domain, to peptides (AAB14420-B14525) which mediate SAM
CC domain function, and to potential modulators of SAM domain function. The
CC SAM domain mediates homo- and heterodimerisation and is found in cell
CC surface receptors, cytoplasmic signalling proteins, transcriptional
CC activators and repressors and chimeric human oncoproteins. For example it
CC is present in the Eph family of receptor tyrosine kinases, the
CC transcription factor TEL, members of the polycomb group of
CC and liprin scaffolding proteins (e.g., RAE28, Scm), the protein kinase Bcr2p
CC and play an important role in both normal and oncogenic signal transduction.
CC The X-ray crystal structure was determined for the SAM domain of the
CC murine ephrin A receptor isoform EphA4 (AAB14400; also known as Sek,
CC Sek1, Cek8, HeK8, and Tyrol1). The SAM domain corresponds to residues 890-
CC 981 of EphA4. The 3D structure of the SAM domain can be used in the
CC determination of the structures of other SAM domain-containing proteins.
CC The SAM domain peptides may be used to identify compounds for drug
CC development and to prepare antibodies. The antibodies can be used to
CC screen for SAM domain-containing proteins, to diagnose and treat
CC disorders associated with aberrant T-cell signalling, and to modulate
CC telomere function. Modulators of SAM domain function may be used to treat
CC diseases associated with inappropriate activity of a protein containing a
CC SAM domain, particularly an Eph receptor. They may be used to treat a
CC cell proliferative disorder such as cancer, atherosclerosis, arthritis
CC and diseases associated with the nervous system, and may be used to
CC modulate angiogenesis. The SAM domain peptides and modulators may be used
CC to modulate the biological activity of an Eph receptor or Eph ligand in a
CC cell, particularly in pathways involved in neuronal development, axonal
CC migration, pathfinding and regeneration. Compositions containing SAM
CC domain modulators may be used in the treatment of neurodegenerative
CC diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's
CC disease, demyelinating diseases such as multiple sclerosis, and
CC amyotrophic lateral sclerosis) and conditions involving trauma and injury
CC to the nervous system (e.g., ischaemia resulting from stroke, and
CC bacterial and viral infection of the nervous system). Sequences AAB14420-
CC B14525 represent peptides which mediate SAM domain function
XX
XX Sequence 6 AA;

Query Match 55.8%; Score 24; DB 3; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 HGRVRP 6
 Db 1 HGRMVP 6

RESULT 12
 ABP98596
 ID ABP98596 standard; peptide; 7 AA.
 XX
 AC ABP98596;
 XX
 DT 18-SEP-2003 (first entry)
 XX
 DE Clone #3 from peptide library.
 XX
 KW Peptide library; cytostatic; tumour cell growth inhibitor;
 KW Transcription factor E2F inhibitor; cell duplication; clone.
 XX
 OS Unidentified.
 XX
 PN WO2003051312-A2.
 XX
 PD 26-JUN-2003.

XX
 PF 17-DEC-2002; 2002WO-US040355.
 XX
 PR 18-DEC-2001; 2001US-0341908P.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX
 PI Scarborough AL, Banerjee D, Bertino JR;
 XX
 DR WPI; 2003-569108/53.
 XX
 PT Composition useful for inhibiting of tumor cell growth comprises an amino
 PT acid peptide or its derivative.
 XX
 PS Disclosure; Page 19; 32pp; English.
 XX
 CC This invention relates to an amino acid peptide believed to be cytostatic
 CC in its action used as a tumour cell growth inhibitor and a transcription
 CC factor E2F inhibitor. The peptides can be used for inhibiting tumour cell
 CC growth and the activity of transcription factor E2F. The compounds
 CC inhibit the transcription factor E2F produced by the phosphorylation of
 CC the tumour suppressor pRb gene by cyclinD/CDK activities, and the
 CC subsequent cell duplication. The present sequence represents a clone from
 CC the random peptide library. Present in the exemplification of the
 CC specification
 XX
 SQ Sequence 7 AA;

Query Match 55.8%; Score 24; DB 7; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 HGRVRPH 7
 Db 1 HAIYRPH 7

RESULT 13
 AAW74241
 ID AAW74241 standard; peptide; 7 AA.
 XX
 AC AAW74241;
 XX
 DT 05-MAY-1999 (first entry)
 XX

DE HJ loop peptide HJ13.
 XX
 KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 1 /note= "acetylated"
 FT Modified-site 7 /note= "amidated"
 XX
 PN WO9853051-A1.
 XX
 PD 26-NOV-1998.
 XX
 PF 20-MAY-1998; 98WO-US010321.
 XX
 PR 21-MAY-1997; 97US-00861153.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Ben-Sasson SA;
 XX
 DR WPI; 1999-070143/06.

XX
 PT New peptide derivatives for modulating protein tyrosine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a protein tyrosine
 PT kinase, used for treating cancers or immune disorders.
 XX
 PS Claim 20; Fig 3; 79pp; English.
 XX
 CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived

XX
 SQ Sequence 7 AA;
 Query Match 53.5%; Score 23; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HGRV 4
 Db 4 HGRV 7
 RESULT 14
 AAW87203
 ID AAW87203 standard; peptide; 6 AA.
 XX
 AC AAW87203;
 XX
 DT 09-FEB-1999 (first entry)
 XX
 DE Peptide determined by the method of the invention.

KW Amino acid determination; molecular mass; fragmentation spectrum;
 XX DNA cloning; anti-body; recombinant; modification; mass spectrometry.
 OS Synthetic.
 XX
 PN GB2325465-A.
 XX
 PD 25-NOV-1998.
 XX
 XX 22-MAY-1998; 98GB-00011196.
 PF
 XX 22-MAY-1997; 97GB-00010582.
 PR
 XX (OXFO-) OXFORD GLYSCSCIENCES UK LTD.
 PA
 XX Parekh RB, Prime SB, Wedd NS, Townsend RR;
 PI
 XX WPI; 1998-571195/49.
 DR
 XX
 XX Peptide sequence determination used in e.g. DNA cloning - by comparing
 PT mass spectra of the unknown peptide with a library of linear chain known
 PT peptide sequences.
 PT
 XX
 XX Example 1; Page 21; 40pp; English.
 PS
 XX The invention relates to a method for determination of the amino acid
 CC sequence of an unknown peptide. The method comprises (a) determining the
 CC molecular mass and an experimental fragmentation spectrum for the peptide
 CC ; (b) comparing the experimental fragmentation spectrum of the peptide
 CC with a theoretical fragmentation spectrum of the unknown
 CC peptide with a theoretical fragmentation spectra calculated for a peptide
 CC library composed of all possible linear sequences of amino acids having a
 CC total mass that corresponds to the molecular mass of the unknown peptide;
 CC and (c) identifying a peptide in the library with a theoretical
 CC fragmentation spectrum that most closely matches the fragmentation
 CC spectrum of the unknown peptide. The method is useful in DNA cloning,
 CC anti-body production, identification of recombinant products, and the
 CC study of post-translational modifications. It allows the sequence of
 CC unknown peptides or proteins with no sub-sequence identity, to be
 CC characterised using mass spectrometry. Sequences AAW87101 to AAW87364
 CC represent a library of linear peptides constructed to exemplify the
 CC method. The isoleucine residue in these peptides can be replaced by
 CC leucine to construct another 264 linear peptides to be included in the
 CC library
 XX
 SQ Sequence 6 AA;
 Query Match 51.2%; Score 22; DB 2; Length 6;
 Best Local Similarity 60.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HGRVR 5
 DB |||:
 2 HGEIR 6
 RESULT 15
 AAW74242
 ID AAW74242 standard; peptide; 7 AA.
 XX
 AC AAW74242;
 XX
 XX 05-MAY-1999 (first entry)
 DT
 XX HJ loop peptide HJ23.1.
 DE
 XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.
 XX
 OS Synthetic.
 OS
 XX Key Location/Qualifiers

FT Modified-site 1 /note= "acetylated"
 FT Modified-site 7 /note= "amidated"
 FT
 XX WO9853051-A1.
 PN
 XX 26-NOV-1998.
 PD
 XX 20-MAY-1998; 98WO-US010321.
 PF
 XX 21-MAY-1997; 97US-00861153.
 PR
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA
 XX Ben-Sasson SA;
 PI
 XX WPI; 1999-070143/06.
 DR
 XX
 XX New peptide derivatives for modulating protein tyrosine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a protein tyrosine
 PT kinase, used for treating cancers or immune disorders.
 PT
 XX
 XX Claim 20; Fig 3; 79pp; English.
 PS
 XX This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived
 XX
 SQ Sequence 7 AA;
 Query Match 51.2%; Score 22; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. NO. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HGRV 4
 DB |||:
 4 HGRI 7
 Search completed: August 3, 2005, 12:03:10
 Job time : 99.3333 secs

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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:26 ; Search time 25 Seconds
(without alignments)

20.902 Million cell updates/sec

Title: US-09-910-582B-3

Perfect score: 43

Sequence: 1 HGRVRPH 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 61165

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pap:*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pap:*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pap:*

4: /cgn2_6/ptodata/1/iaa/6B COMB.pap:*

5: /cgn2_6/ptodata/1/iaa/PCRTUS COMB.pap:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	7	3	US-09-326-718-3
2	24	55.8	6	4	US-09-500-700-101
3	23	53.5	7	4	US-08-861-153A-26
4	22	51.2	6	4	US-08-877-605-103
5	22	51.2	7	4	US-09-202-329-21
6	22	51.2	7	4	US-08-861-153A-34
7	21	48.8	5	4	US-08-839-743-27
8	20	46.5	4	2	US-08-177-109A-22
9	20	46.5	4	2	US-08-687-706-22
10	20	46.5	6	1	US-08-225-224-53
11	20	46.5	6	3	US-08-722-258-53
12	20	46.5	6	3	US-09-196-934-4
13	20	46.5	6	4	US-08-877-605-116
14	20	46.5	6	5	PCT-US95-04468-53
15	20	46.5	7	1	US-08-074-210-3
16	20	46.5	7	1	US-08-074-210-5
17	20	46.5	7	2	US-08-177-109A-55
18	20	46.5	7	2	US-08-687-706-55
19	20	46.5	7	3	US-09-139-802-85
20	20	46.5	7	3	US-09-025-819-3
21	20	46.5	7	3	US-09-031-902-5
22	20	46.5	7	3	US-09-031-902-6
23	20	46.5	7	3	US-09-031-902-11
24	20	46.5	7	3	US-09-031-902-12
25	20	46.5	7	4	US-09-808-126-3
26	20	46.5	7	4	US-09-803-951-3
27	20	46.5	7	4	US-09-659-786-85
28	20	46.5	7	4	US-08-926-914-85
29	20	46.5	7	5	PCT-US94-06502A-4
30	20	46.5	7	5	PCT-US94-06502A-5
31	19	44.2	4	4	US-10-132-920B-52
32	19	44.2	4	4	US-09-700-696C-49
33	19	44.2	5	2	US-08-350-260A-410
34	19	44.2	5	4	US-08-055-006-47
35	19	44.2	5	4	US-09-104-337A-410
36	19	44.2	6	1	US-08-665-220-18
37	19	44.2	6	2	US-08-618-408B-18
38	19	44.2	6	2	US-08-893-853-13
39	19	44.2	6	3	US-09-113-921-13
40	19	44.2	6	3	US-09-257-218-29
41	19	44.2	6	3	US-09-311-760-29
42	19	44.2	6	3	US-09-291-692-18
43	19	44.2	6	3	US-09-561-756-67
44	19	44.2	6	3	US-09-227-721-67
45	19	44.2	6	4	US-09-155-613A-44
46	19	44.2	6	4	US-08-865-579-29
47	19	44.2	6	4	US-09-451-067-13
48	19	44.2	6	4	US-10-059-749-29
49	19	44.2	6	4	US-08-877-605-31
50	19	44.2	6	4	US-08-877-605-32
51	19	44.2	6	4	US-08-877-605-33
52	19	44.2	6	4	US-08-877-605-34
53	19	44.2	6	4	US-08-877-605-35
54	19	44.2	6	4	US-08-877-605-36
55	19	44.2	6	4	US-09-954-697-67
56	19	44.2	6	4	US-09-352-768-18
57	19	44.2	7	2	US-08-726-306A-20
58	19	44.2	7	4	US-09-007-288B-48
59	18	41.9	6	4	US-08-877-605-127
60	17.5	40.7	5	6	5217869-57
61	17.5	40.7	5	6	5217869-57
62	17	39.5	5	1	US-08-467-940-2
63	17	39.5	5	1	US-08-633-772-2
64	17	39.5	5	1	US-08-259-550A-24
65	17	39.5	5	3	US-08-871-572B-17
66	17	39.5	6	1	US-08-037-486-4
67	17	39.5	6	1	US-08-014-979-93
68	17	39.5	6	1	US-08-249-371-6
69	17	39.5	6	1	US-08-259-550A-3
70	17	39.5	6	3	US-09-135-021-74
71	17	39.5	6	3	US-08-218-369-3
72	17	39.5	6	4	US-09-155-613A-75
73	17	39.5	6	4	US-08-877-605-141
74	17	39.5	6	4	US-09-904-599A-3
75	17	39.5	6	5	PCT-US95-03742-3
76	17	39.5	6	5	PCT-US95-06451-6
77	17	39.5	7	1	US-07-977-234C-9
78	17	39.5	7	1	US-08-366-276-4
79	17	39.5	7	1	US-08-346-333-86
80	17	39.5	7	1	US-08-259-550A-25
81	17	39.5	7	1	US-08-259-550A-26
82	17	39.5	7	1	US-08-259-550A-45
83	17	39.5	7	3	US-08-640-737-35
84	17	39.5	7	3	US-09-031-902-8
85	17	39.5	7	4	US-09-485-534-5
86	17	39.5	7	5	PCT-US91-07506-86
87	16	37.2	3	1	US-08-037-486-11
88	16	37.2	4	1	US-08-037-486-5
89	16	37.2	4	1	US-08-259-550A-4
90	16	37.2	4	2	US-08-244-496-35
91	16	37.2	4	2	US-08-244-496-47
92	16	37.2	5	2	US-08-244-496-51
93	16	37.2	5	2	US-08-348-353-8
94	16	37.2	5	2	US-08-465-965-8
95	16	37.2	5	3	US-08-465-966-8
96	16	37.2	5	3	US-09-298-924-42
97	16	37.2	5	4	US-09-459-958-9
98	16	37.2	6	1	US-08-014-979-75
99	16	37.2	6	1	US-08-014-979-77
100	16	37.2	6	1	US-08-471-052A-164

ALIGNMENTS

RESULT 1

US-09-326-718-3
; Sequence 3, Application US/09326718
; Patent No. 6303573
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: MacKenna, Deirdre A.
; TITLE OF INVENTION: Heart Homing Peptides and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-LJ 3512
; CURRENT APPLICATION NUMBER: US/09/326,718
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-326-718-3

Query Match 100.0%; Score 43; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGRVRPH 7
Db 1 HGRVRPH 7

RESULT 2

US-09-500-700-101
; Sequence 101, Application US/09500700
; Patent No. 6790941
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: BARBAS III, Carlos F.
; APPLICANT: GOTTESFELD, Joel M.
; APPLICANT: WRIGHT, Peter E.
; TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR
; FILE REFERENCE: SCRIPI160-4
; CURRENT APPLICATION NUMBER: US/09/500,700
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 08/863,813
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: US 08/676,318
; PRIOR FILING DATE: 1996-12-30
; PRIOR APPLICATION NUMBER: PCT/US95/00829
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: US 08/312,604
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: US 08/183,119
; PRIOR FILING DATE: 1994-01-18
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Modified sequence of finger 2 of zif268
US-09-500-700-101

Query Match 55.8%; Score 24; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VRPH 7
Db 1 VRPH 4

RESULT 3

US-08-861-153A-26
; Sequence 26, Application US/08861153A
; Patent No. 6723694
; GENERAL INFORMATION:
; APPLICANT: BEN-SASSON, Shmuel A
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY MODULATE INTRACELLULAR SIGNALING
; FILE REFERENCE: BEN-SASSON-1
; CURRENT APPLICATION NUMBER: US/08/861,153A
; CURRENT FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: N-acetyl-Leucine
; NAME/KEY: MOD RES
; LOCATION: (7)-(7)
; OTHER INFORMATION: Valine-NH2
US-08-861-153A-26

Query Match 53.5%; Score 23; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGRV 4
Db 4 HGRV 7

RESULT 4

US-08-877-605-103
; Sequence 103, Application US/08877605
; Patent No. 6582965
; GENERAL INFORMATION:
; APPLICANT: Robert Townsend
; APPLICANT: Raj Parekh
; APPLICANT: Sally Prime
; APPLICANT: Nick Webb
; TITLE OF INVENTION: A METHOD FOR DE NOVO PEPTIDE SEQUENCE DETERMINATION
; FILE REFERENCE: 9195-004
; CURRENT APPLICATION NUMBER: US/08/877,605
; CURRENT FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 103
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide X Library
US-08-877-605-103

Query Match 51.2%; Score 22; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HGRVR 5
Db 2 HGEIR 6

RESULT 5

US-09-202-329-21
; Sequence 21, Application US/09202329A
; Patent No. 6676944
; GENERAL INFORMATION:
; APPLICANT: Dalton, John P
; APPLICANT: Andrews, Stuart J
; TITLE OF INVENTION: Vaccine containing a peroxiredoxin and/or a B-tubulin
; FILE REFERENCE: 1181-243
; CURRENT APPLICATION NUMBER: US/09/202,329A
; PRIOR FILING DATE: 1999-02-19
; EARLIER APPLICATION NUMBER: GB 9612214.8
; EARLIER FILING DATE: 1996-06-11
; EARLIER APPLICATION NUMBER: PCT/GB97/01573
; EARLIER FILING DATE: 1997-06-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Fasciola hepatica
US-09-202-329-21

Query Match 51.2%; Score 22; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HGRVRP 6
|||
Db 1 HGEVCP 6

RESULT 6
US-08-861-153A-34
; Sequence 34, Application US/08861153A
; Patent No. 6723694
; GENERAL INFORMATION:
; APPLICANT: BEN-SASSON, Shmuel A
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY MODULATE INTRACELLULAR SIGNALING
; FILE REFERENCE: BEN-SASSON=1
; CURRENT APPLICATION NUMBER: US/08/861,153A
; CURRENT FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-Acetyl-Isoleucine
; NAME/KEY: MOD RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: Isoleucine-NH2
US-08-861-153A-34

Query Match 51.2%; Score 22; DB 4; Length 7;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGRV 4
|||
Db 4 HGRI 7

RESULT 7
US-09-839-743-27
; Sequence 27, Application US/09839743
; Patent No. 6472211
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher

; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. 6472211el Transcription Enhancer Element and
; FILE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-839-743-27

Query Match 48.8%; Score 21; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRVRP 6
|||
Db 1 GRPRP 5

RESULT 8
US-08-177-109A-22
; Sequence 22, Application US/08177109A
; Patent No. 5863615
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/177,109A
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
US-08-177-109A-22

Query Match 46.5%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RPH 7
Db 1 RPH 3

RESULT 9

US-08-687-706-22
; Sequence 22, Application US/08687706
; Patent No. 5928892
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,706
; FILING DATE: 26-JUL-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 08/177,109
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107 DIV
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
US-08-687-706-22

Query Match 46.5%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RPH 7
Db 1 RPH 3

RESULT 10

US-08-225-224-53
; Sequence 53, Application US/08225224
; Patent No. 5635599
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: KREITMAN, Robert J.
; TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
; TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,224
; FILING DATE: 8-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-225-224-53

Query Match 46.5%; Score 20; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RPH 7
Db 1 RPH 3

RESULT 11

US-08-722-258-53
; Sequence 53, Application US/08722258
; Patent No. 6011002
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Kreitman, Robert J.
; APPLICANT: Puri, Raj K.
; TITLE OF INVENTION: Circularly Permuted Ligands and
; TITLE OF INVENTION: Circularly Permuted Chimeric Molecules
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,258
; FILING DATE: 08-JAN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/04468
; FILING DATE: 08-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/225,224
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:


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; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-193100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-722-258-53

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Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RPH 7
Db 1 RPH 3

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US-09-196-934-4
; Sequence 4, Application US/09196934
; Patent No. 6191256
; GENERAL INFORMATION:
; APPLICANT: Chen, Li Ang
; APPLICANT: Beutner, Joseph A.
; APPLICANT: Carbone, Ruben G.
; TITLE OF INVENTION: Recombinant Factor VIII Binding Peptides
; FILE REFERENCE: MSB-7251
; CURRENT APPLICATION NUMBER: US/09/196,934
; CURRENT FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-196-934-4

Query Match 46.5%; Score 20; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RPH 7
Db 2 RPH 4

RESULT 13
US-08-877-605-116
; Sequence 116, Application US/08877605
; Patent No. 6582965
; GENERAL INFORMATION:
; APPLICANT: Robert Townsend
; APPLICANT: Raj Parekh
; APPLICANT: Sally Prime
; APPLICANT: Nick Webb
; TITLE OF INVENTION: A METHOD FOR DE NOVO PEPTIDE SEQUENCE DETERMINATION
; FILE REFERENCE: 9195-004
; CURRENT APPLICATION NUMBER: US/08/877,605
; CURRENT FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 116
; LENGTH: 6
; TYPE: PRT
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Peptide X Library
US-08-877-605-116

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Qy 1 HGRVR 5
Db 2 HGHIR 6

RESULT 14
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; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
; TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS
; NUMBER OF SEQUENCES: 59
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04468
; FILING DATE: 07-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/225,224
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-193-1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-04468-53

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Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RPH 7
Db 1 RPH 3

RESULT 15
US-08-074-210-3
; Sequence 3, Application US/08074210
; Patent No. 5482930
; GENERAL INFORMATION:
; APPLICANT: Wei, Edward T.
; APPLICANT: Thomas, Holly A.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOSITION AND METHOD
; TITLE OF INVENTION: WITH DES-TYR DYNORPHIN AND ANALOGUES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Haue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
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; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/074,210
; FILING DATE: 19930609
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2500.72
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 362-5556
; TELEFAX: (415) 362-5418
; TELEX: 278638 MGPS
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-074-210-3
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Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVRP 6
Db 2 RIRP 5
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Job time : 27 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2005, 11:57:01 ; Search time 89.3333 Seconds
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Title: US-09-910-582B-3
Perfect score: 43
Sequence: 1 HGRVRPH 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

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Listing first 100 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	43	100.0	7	17	US-10-838-289-35
4	31	72.1	6	15	US-10-381-734-25
5	25	58.1	5	15	US-10-381-734-14
6	25	58.1	7	15	US-10-381-734-1
7	25	58.1	7	15	US-10-381-734-8
8	25	58.1	7	15	US-10-381-734-16
9	25	58.1	7	15	US-10-381-734-23
10	24	55.8	6	10	US-09-500-700-101
11	24	55.8	6	17	US-10-941-069-101
					Sequence 2, Appli
					Sequence 3, Appli
					Sequence 35, Appl
					Sequence 25, Appl
					Sequence 14, Appl
					Sequence 1, Appli
					Sequence 8, Appli
					Sequence 16, Appl
					Sequence 23, Appl
					Sequence 101, App
					Sequence 101, App

12	22	51.2	7	10	US-09-202-329-21	Sequence 21, Appl
13	21	48.8	4	18	US-10-892-402-102	Sequence 102, App
14	21	48.8	5	9	US-09-839-743-27	Sequence 27, Appl
15	20.5	47.7	7	16	US-10-363-204-55	Sequence 55, Appl
16	20	46.5	4	17	US-10-476-861A-10	Sequence 10, Appl
17	20	46.5	4	17	US-10-476-861A-52	Sequence 52, Appl
18	20	46.5	4	17	US-10-476-861A-127	Sequence 127, App
19	20	46.5	6	14	US-10-372-076-151	Sequence 151, App
20	20	46.5	6	16	US-10-677-074-151	Sequence 151, App
21	21	46.5	6	16	US-10-672-396-15	Sequence 15, App
22	20	46.5	7	9	US-09-803-951-3	Sequence 3, Appli
23	20	46.5	7	9	US-09-765-086-85	Sequence 85, Appl
24	20	46.5	7	10	US-09-978-309A-62	Sequence 62, Appl
25	20	46.5	7	11	US-09-855-604-23	Sequence 23, Appl
26	20	46.5	7	12	US-09-855-604-23	Sequence 23, Appl
27	20	46.5	7	14	US-10-264-374-85	Sequence 85, Appl
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31	20	46.5	7	17	US-10-838-289-846	Sequence 846, App
32	20	46.5	7	17	US-10-898-675-62	Sequence 62, Appl
33	20	46.5	7	17	US-10-892-831-62	Sequence 62, Appl
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35	19	44.2	4	15	US-10-438-181A-52	Sequence 52, Appl
36	19	44.2	4	17	US-10-920-788-49	Sequence 49, Appl
37	19	44.2	5	15	US-10-436-549-174	Sequence 174, App
38	19	44.2	5	16	US-10-712-425-174	Sequence 174, App
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40	19	44.2	6	8	US-08-865-579-29	Sequence 29, Appl
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49	19	44.2	6	15	US-10-668-955-18	Sequence 18, Appl
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59	19	44.2	7	16	US-10-727-335-10	Sequence 10, Appl
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61	19	44.2	7	17	US-10-235-043-70	Sequence 46, Appl
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63	18	41.9	6	18	US-10-975-157-36	Sequence 36, Appl
64	18	41.9	7	10	US-09-954-385-408	Sequence 408, App
65	18	41.9	7	10	US-09-990-832C-44	Sequence 44, Appl
66	18	41.9	7	14	US-10-211-088-180	Sequence 180, App
67	18	41.9	7	14	US-10-052-578-217	Sequence 217, App
68	18	41.9	7	14	US-10-053-520-217	Sequence 217, App
69	18	41.9	7	14	US-10-053-498B-217	Sequence 217, App
70	18	41.9	7	15	US-10-258-146A-75	Sequence 75, Appl
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72	18	41.9	7	16	US-10-258-144-110	Sequence 110, App
73	18	41.9	7	16	US-10-727-335-37	Sequence 37, Appl
74	18	41.9	7	17	US-10-783-311-343	Sequence 343, App
75	18	41.9	7	17	US-10-912-512-408	Sequence 408, App
76	18	41.9	7	17	US-10-235-043-408	Sequence 408, App
77	18	41.9	7	18	US-10-975-157-35	Sequence 35, Appl
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79	17.5	40.7	7	14	US-10-052-578-276	Sequence 276, App
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82	17.5	40.7	7	15	US-10-258-146A-134	Sequence 134, App
83	17.5	40.7	7	15	US-10-328-953-279	Sequence 279, App
84	17.5	40.7	7	16	US-10-258-144-169	Sequence 169, App

85 17 39.5 4 18 US-10-892-402-1114 Sequence 114, App
86 17 39.5 6 9 US-09-904-599A-3 Sequence 3, Appl
87 17 39.5 6 9 US-09-847-101B-46 Sequence 46, Appl
88 17 39.5 6 13 US-10-156-820-75 Sequence 75, Appl
89 17 39.5 6 15 US-10-414-523-12 Sequence 12, Appl
90 17 39.5 6 15 US-10-297-229-13 Sequence 13, Appl
91 17 39.5 6 16 US-10-699-088-580 Sequence 580, App
92 17 39.5 6 16 US-10-699-088-758 Sequence 758, App
93 17 39.5 6 16 US-10-699-088-759 Sequence 759, App
94 17 39.5 6 16 US-10-699-088-1057 Sequence 1057, App
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96 17 39.5 6 16 US-10-699-113-146 Sequence 146, App
97 17 39.5 6 16 US-10-699-113-147 Sequence 147, App
98 17 39.5 6 16 US-10-699-113-580 Sequence 580, App
99 17 39.5 6 16 US-10-699-113-758 Sequence 758, App
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ALIGNMENTS

RESULT 1
US-09-782-650-2
; Sequence 2, Application US/09782650
; Patent No. US2002001950A1
; GENERAL INFORMATION:
; APPLICANT: Levine, Arnold J.
; APPLICANT: Mitterer, Artur
; APPLICANT: Falkner, Falko-Guenter
; APPLICANT: Scheiflinger, Friedrich
; APPLICANT: Dornier, Friedrich
; APPLICANT: Edwards LifeSciences Corporation
; TITLE OF INVENTION: Targeted Angiogenesis
; FILE REFERENCE: 2053D-000611US
; CURRENT APPLICATION NUMBER: US/09782, 650
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: US 09/324, 079
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 09/327, 045
; PRIOR FILING DATE: 1999-06-07
; PRIOR APPLICATION NUMBER: PCT/US00/14988
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:targeting
; OTHER INFORMATION: molecule
US-09-782-650-2

Query Match 100.0%; Score 43; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGRVRPH 7
Db 1 HGRVRPH 7

RESULT 2
US-09-910-582B-3
; Sequence 3, Application US/09910582B
; Publication No. US20030045476A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Mackenna, Deidre A.
; TITLE OF INVENTION: Heart Homing Conjugates
; FILE REFERENCE: P-LJ 4857
; CURRENT APPLICATION NUMBER: US/09/910,582B
; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 09/326,718
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-910-582B-3

Query Match 100.0%; Score 43; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGRVRPH 7
Db 1 HGRVRPH 7

RESULT 3
US-10-838-289-35
; Sequence 35, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jimming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; TITLE OF INVENTION: NANOSHELLS
; FILE REFERENCE: CWRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Heart homing peptide
US-10-838-289-35

Query Match 100.0%; Score 43; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGRVRPH 7
Db 1 HGRVRPH 7

RESULT 4
US-10-381-734-25
; Sequence 25, Application US/10381734
; Publication No. US20040092434A1
; GENERAL INFORMATION:
; APPLICANT: BETZ, NATACHA
; APPLICANT: BIKPALVI, ANDREAS
; APPLICANT: DELERIS, GERARD
; TITLE OF INVENTION: CYCLOPEPTIDES, A METHOD FOR THEIR PREPARATION AND THEIR USE AS IN
; TITLE OF INVENTION: OR ACTIVATORS OF ANGIOGENESIS
; FILE REFERENCE: 235834US0XPCT
; CURRENT APPLICATION NUMBER: US/10/381,734
; CURRENT FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: PCT/FR01/03049
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: FR 00 012654
; PRIOR FILING DATE: 2000-10-04

; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Cyclic Peptide
US-10-381-734-25

Query Match 72.1%; Score 31; DB 15; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GVRVPH 7
|:|:
Db 1 GRIKPH 6

RESULT 5

US-10-381-734-14
; Sequence 14, Application US/10381734
; Publication No. US20040092434A1
; GENERAL INFORMATION:
; APPLICANT: BETZ, NATACHA
; APPLICANT: BIKFALVI, ANDREAS
; APPLICANT: DELERIS, GERARD

; TITLE OF INVENTION: CYCLOPEPTIDES, A METHOD FOR THEIR PREPARATION AND THEIR USE AS IN
; FILE REFERENCE: 235834USOXPCT
; CURRENT APPLICATION NUMBER: US/10/381,734
; CURRENT FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: PCT/FR01/03049
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: FR 00 012654
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-381-734-14

Query Match 58.1%; Score 25; DB 15; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVRPH 7
|:|:
Db 1 RIKPH 5

RESULT 6

US-10-381-734-1
; Sequence 1, Application US/10381734
; Publication No. US20040092434A1
; GENERAL INFORMATION:
; APPLICANT: BETZ, NATACHA
; APPLICANT: BIKFALVI, ANDREAS
; APPLICANT: DELERIS, GERARD

; TITLE OF INVENTION: CYCLOPEPTIDES, A METHOD FOR THEIR PREPARATION AND THEIR USE AS IN
; FILE REFERENCE: 235834USOXPCT
; CURRENT APPLICATION NUMBER: US/10/381,734
; CURRENT FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: PCT/FR01/03049
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: FR 00 012654
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-381-734-1

Query Match 58.1%; Score 25; DB 15; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVRPH 7
|:|:
Db 1 RIKPH 5

RESULT 7

US-10-381-734-8
; Sequence 8, Application US/10381734
; Publication No. US20040092434A1
; GENERAL INFORMATION:
; APPLICANT: BETZ, NATACHA
; APPLICANT: BIKFALVI, ANDREAS
; APPLICANT: DELERIS, GERARD

; TITLE OF INVENTION: CYCLOPEPTIDES, A METHOD FOR THEIR PREPARATION AND THEIR USE AS IN
; FILE REFERENCE: 235834USOXPCT
; CURRENT APPLICATION NUMBER: US/10/381,734
; CURRENT FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: PCT/FR01/03049
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: FR 00 012654
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Cyclic Peptide
US-10-381-734-8

Query Match 58.1%; Score 25; DB 15; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVRPH 7
|:|:
Db 1 RIKPH 5

RESULT 8

US-10-381-734-16
; Sequence 16, Application US/10381734
; Publication No. US20040092434A1
; GENERAL INFORMATION:
; APPLICANT: BETZ, NATACHA
; APPLICANT: BIKFALVI, ANDREAS
; APPLICANT: DELERIS, GERARD

; TITLE OF INVENTION: CYCLOPEPTIDES, A METHOD FOR THEIR PREPARATION AND THEIR USE AS IN
; FILE REFERENCE: 235834USOXPCT
; CURRENT APPLICATION NUMBER: US/10/381,734
; CURRENT FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: PCT/FR01/03049
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: FR 00 012654
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-381-734-16

Query Match          58.1%; Score 25; DB 15; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 RVRPH 7
      |::||
Db      1 RIKPH 5

RESULT 9
US-10-381-734-23
; Sequence 23, Application US/10381734
; Publication No. US20040092434A1
; GENERAL INFORMATION:
; APPLICANT: BETZ, NATACHA
; APPLICANT: BIKFALVI, ANDREAS
; APPLICANT: DELERIS, GERARD
; TITLE OF INVENTION: CYCLOPEPTIDES, A METHOD FOR THEIR PREPARATION AND THEIR USE AS IN
; TITLE OF INVENTION: OR ACTIVATORS OF ANGIOGENESIS
; FILE REFERENCE: 235834USOXPC
; CURRENT APPLICATION NUMBER: US/10/381,734
; CURRENT FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: PCT/FR01/03049
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: FR 00 012654
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Cyclic Peptide
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: (D) Phe
US-10-381-734-23

Query Match          58.1%; Score 25; DB 15; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 RVRPH 7
      |::||
Db      2 RIKPH 6

RESULT 10
US-09-500-700-101
; Sequence 101, Application US/09500700
; Publication No. US20030059767A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: BARBAS III, Carlos F.
; APPLICANT: GOTTESFELD, Joel M.
; APPLICANT: WRIGHT, Peter E.
; TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR
; FILE REFERENCE: SCRIPT160-4
; CURRENT APPLICATION NUMBER: US/09/500,700
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 08/863,813
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: US 08/676,318
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; PRIOR FILING DATE: 1996-12-30
; PRIOR APPLICATION NUMBER: PCT/US95/00829
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: US 08/312,604
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: US 08/183,119
; PRIOR FILING DATE: 1994-01-18
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Modified sequence of finger 2 of zif268
US-09-500-700-101

Query Match          55.8%; Score 24; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 VRPH 7
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Db      1 VRPH 4

RESULT 11
US-10-941-069-101
; Sequence 101, Application US/10941069
; Publication No. US20050084885A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: BARBAS III, Carlos F.
; APPLICANT: GOTTESFELD, Joel M.
; APPLICANT: WRIGHT, Peter E.
; TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR
; FILE REFERENCE: SCRIPT1160-4
; CURRENT APPLICATION NUMBER: US/10/941,069
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/09/500,700
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 08/863,813
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: US 08/676,318
; PRIOR FILING DATE: 1996-12-30
; PRIOR APPLICATION NUMBER: PCT/US95/00829
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: US 08/312,604
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: US 08/183,119
; PRIOR FILING DATE: 1994-01-18
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Modified sequence of finger 2 of zif268
US-10-941-069-101

Query Match          55.8%; Score 24; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 VRPH 7
      ||||
Db      1 VRPH 4

RESULT 12
US-09-202-329-21
; Sequence 21, Application US/09202329A
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; Publication No. US20030124137A1
; GENERAL INFORMATION:
; APPLICANT: Dalton, John P
; APPLICANT: Andrews, Stuart J
; TITLE OF INVENTION: Vaccine containing a peroxiredoxin and/or a B-tubulin
; FILE REFERENCE: 1181-243
; CURRENT APPLICATION NUMBER: US/09/202,329A
; CURRENT FILING DATE: 1999-02-19
; EARLIER APPLICATION NUMBER: GB 9612214.8
; EARLIER FILING DATE: 1996-06-11
; EARLIER APPLICATION NUMBER: PCT/GB97/01573
; EARLIER FILING DATE: 1997-06-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Fasciola hepatica
US-09-202-329-21

Query Match      51.2%; Score 22; DB 10; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HGRVRP 6
   ||||
Db 1 HGEVCP 6

RESULT 13
US-10-892-402-102
; Sequence 102, Application US/10892402
; Publication No. US20050153306A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winessinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-102

Query Match      48.8%; Score 21; DB 18; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVRP 6
   ||||
Db 1 RVRP 4

RESULT 14
US-09-839-743-27
; Sequence 27, Application US/09839743
; Patent No. US20020146824A1
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter

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; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. US20020146824A1el Transcription Enhancer Element and
; FILE REFERENCE: SALKINS 008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-839-743-27

Query Match      48.8%; Score 21; DB 9; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRVRP 6
   ||||
Db 1 GRPRP 5

RESULT 15
US-10-363-204-55
; Sequence 55, Application US/10363204
; Publication No. US20040170955A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: US/10/363,204
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(7)
; OTHER INFORMATION: synthetic construct
US-10-363-204-55

Query Match      47.7%; Score 20.5; DB 16; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.6e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 HGR-VRP 6
   ||||
Db 1 HGOVRP 7

Search completed: August 3, 2005, 12:14:01
Job time : 91.3333 secs

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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:26 ; Search time 19 Seconds
(without alignments)
35.448 Million cell updates/sec

Title: US-09-910-582B-4

Perfect score: 29

Sequence: 1 VLVVTSS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	58.6	5	2	B44817
2	17	58.6	5	2	D44817
3	15	51.7	5	2	H44817
4	15	51.7	5	2	F44817
5	14	48.3	4	2	B43848
6	14	48.3	7	2	E30608
7	13	44.8	7	2	A30812
8	13	44.8	7	4	A58725
9	12	41.4	6	2	A49808
10	11	37.9	7	2	S70335
11	10	34.5	4	2	A27897
12	10	34.5	4	2	A40135
13	10	34.5	5	2	B31836
14	10	34.5	5	2	E42364
15	10	34.5	7	2	PQ0728
16	10	34.5	7	2	A25265
17	9	31.0	4	2	S17255
18	9	31.0	5	2	JT0520
19	9	31.0	6	2	B61512
20	9	31.0	6	2	A31263
21	9	31.0	6	2	P70593
22	9	31.0	6	2	S60293
23	9	31.0	7	1	XEYDGD
24	9	31.0	7	2	PQ0727
25	9	31.0	7	2	FC1316
26	9	31.0	7	2	P70269
27	9	31.0	7	2	FX0008
28	8	27.6	3	3	PQ0010
29	8	27.6	3	3	P70622

30	8	27.6	4	2	T46627	hypothetical prote
31	8	27.6	4	2	PT0696	T-cell receptor be
32	8	27.6	4	2	PT0645	T-cell receptor be
33	8	27.6	4	2	PT0712	T-cell receptor be
34	8	27.6	4	2	PT0698	T-cell receptor be
35	8	27.6	4	2	PT0551	T-cell receptor be
36	8	27.6	4	2	PT0897	T-cell receptor be
37	8	27.6	5	2	C41225	copper resistance
38	8	27.6	5	2	E60274	major protein anti
39	8	27.6	5	2	T10954	hypothetical prote
40	8	27.6	5	2	S55237	zinc-binding prote
41	8	27.6	5	2	A37114	hypoxanthine phosph
42	8	27.6	5	2	I50385	myosin light chain
43	8	27.6	5	2	PT0278	Ig heavy chain CRD
44	8	27.6	5	2	PT0308	Ig heavy chain CRD
45	8	27.6	5	2	PT0596	T-cell receptor be
46	8	27.6	5	2	PT0610	T-cell receptor be
47	8	27.6	5	2	PT0597	T-cell receptor be
48	8	27.6	5	2	PT0729	T-cell receptor be
49	8	27.6	5	2	PT0624	T-cell receptor be
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55	8	27.6	5	2	PT0535	T-cell receptor be
56	8	27.6	5	2	PT0699	T-cell receptor be
57	8	27.6	5	2	PT0561	T-cell receptor be
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62	8	27.6	5	2	PT0713	T-cell receptor be
63	8	27.6	5	2	I40698	biotin B - Citropa
64	8	27.6	5	2	PT0644	T-cell receptor be
65	8	27.6	5	2	PT0600	T-cell receptor be
66	8	27.6	5	2	PT0686	T-cell receptor be
67	8	27.6	5	2	PT0601	T-cell receptor be
68	8	27.6	5	2	PT0565	T-cell receptor be
69	8	27.6	5	2	PT0714	T-cell receptor be
70	8	27.6	5	2	PT0701	T-cell receptor be
71	8	27.6	5	2	PT0717	T-cell receptor be
72	8	27.6	6	2	A35890	RNA-directed DNA p
73	8	27.6	6	2	A60986	N-formyl oligopept
74	8	27.6	6	2	I59142	platelet-derived g
75	8	27.6	6	2	PT0510	T-cell receptor be
76	8	27.6	6	2	PT0531	T-cell receptor be
77	8	27.6	6	2	PT0532	T-cell receptor be
78	8	27.6	6	2	PT0519	T-cell receptor be
79	8	27.6	6	2	PT0599	T-cell receptor be
80	8	27.6	6	2	PT0637	T-cell receptor be
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90	8	27.6	6	2	PT0533	T-cell receptor be
91	8	27.6	6	2	PT0720	T-cell receptor be
92	8	27.6	6	2	PT0560	T-cell receptor be
93	8	27.6	6	2	PT0550	T-cell receptor be
94	8	27.6	6	2	PT0718	T-cell receptor be
95	8	27.6	6	2	PT0589	T-cell receptor be
96	8	27.6	6	2	PT0693	T-cell receptor be
97	8	27.6	6	2	PT0715	T-cell receptor be
98	8	27.6	6	2	PT0730	T-cell receptor be
99	8	27.6	6	2	A61068	locustakinin - mig
100	8	27.6	6	2	A49792	acetylaminocyl-pept

ALIGNMENTS

RESULT 1
B44817
34.5K structural protein - Leuconostoc oenos phase P2t11-15 (fragment)
C;Species: Leuconostoc oenos phase P2t11-15
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: B44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: B44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70342)

Query Match 58.6%; Score 17; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVTSS 7
: |||
Db 1 LATSS 5

RESULT 2
D44817
35K structural protein - Leuconostoc oenos phase PAt5-12 (fragment)
C;Species: Leuconostoc oenos phase PAt5-12
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: D44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: D44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70340)

Query Match 58.6%; Score 17; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVTSS 7
: |||
Db 1 LATSS 5

RESULT 4
F44817
34.5K structural protein - Leuconostoc oenos phase P54 (fragment)
C;Species: Leuconostoc oenos phase P54
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: F44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: F44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70335)

Query Match 51.7%; Score 15; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVTSS 7
: |||
Db 1 MATSS 5

RESULT 5
B43848
cell surface adhesin for heparan sulfate, 60K - Staphylococcus aureus (fragment)
C;Species: Staphylococcus aureus
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 24-Feb-1995
C;Accession: B43848
R;Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.
Infect. Immun. 60, 899-906, 1992
A;Title: Binding of heparan sulfate to Staphylococcus aureus.
A;Reference number: A43848; MUID:92176005; PMID:1541563
A;Accession: B43848
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <LIA>
A;Note: sequence extracted from NCBI backbone (NCBIP:85444)

Query Match 48.3%; Score 14; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLVT 5
: |||
Db 1 MLVT 4

RESULT 6
E30608
IG kappa chain V-III region (Gag) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
C;Accession: E30608
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies.
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: E30608
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <GON>
C;Keywords: heterotetramer; immunoglobulin

Query Match 48.3%; Score 14; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VVLVTS 6
: || |

RESULT 3
H44817
34.5K structural protein - Leuconostoc oenos phase P32 (fragment)
C;Species: Leuconostoc oenos phase P32
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: H44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: H44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70332)

Query Match 51.7%; Score 15; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVTSS 7
: |||
Db 1 MATSS 5

RESULT 6
E30608
IG kappa chain V-III region (Gag) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
C;Accession: E30608
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies.
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: E30608
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <GON>
C;Keywords: heterotetramer; immunoglobulin

Query Match 48.3%; Score 14; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VVLVTS 6
: || |

Db 2 IVLTQS 7

RESULT 7
A30812
sex pheromone cCF10 - Enterococcus faecalis
C;Species: Enterococcus faecalis
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: A30812
R;Mori, M.; Sakagami, Y.; Ishii, Y.; Isogai, A.; Kitada, C.; Fujino, M.; Adsit, J.C.; Du
J. Biol. Chem. 263, 14574-14578, 1988
A;Title: Structure of cCF10, a peptide sex pheromone which induces conjugative transfer
A;Reference number: A30812; MUID:89008313; PMID:3139658
A;Molecule type: protein
A;Residues: 1-7 <MOR>
A;Cross-references: UNIPROT:P20104

Query Match 44.8%; Score 13; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVT 5
|||
Db 1 LVT 3

RESULT 8
A58725
virotoxin - destroying angel
C;Species: Amanita virosa (destroying angel)
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: A58725
R;Paulstich, H.; Buku, A.; Bodenmueller, H.; Wieland, T.
Biochemistry 19, 334-343, 1980
A;Title: Virotoxins: actin-binding cyclic peptides of Amanita virosa mushrooms.
A;Reference number: A58725; MUID:6893271; PMID:6893271
A;Accession: A58725
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <PAU>
C;Keywords: D-amino acid; hydroxyproline; toxin; unencoded polypeptide
F;1/7/Cross-link: cyclopeptide (Val-Leu) #status experimental
F;2/Modified site: D-threonine (Thr) #status experimental
F;3/Modified site: D-serine (Ser) #status experimental
F;4/Modified site: (3R,4S)-3,4-dihydroxyproline (Pro) #status experimental
F;6/Modified site: 2'-methylsulfonyltryptophan (Trp) #status experimental
F;7/Modified site: 4,5-dihydroxyleucine (Leu) #status experimental

Query Match 44.8%; Score 13; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VTS 6
|||
Db 1 VTS 3

RESULT 9
I49808
D-SP2.5 region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I49808
R;Kurosawa, Y.; Tonegawa, S.
J. Exp. Med. 155, 201-218, 1982
A;Title: Organization, structure, and assembly of immunoglobulin heavy chain diversity D
A;Reference number: I49808; MUID:82099936; PMID:6798155
A;Accession: I49808
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: GB:J00432; NID:G194370; PIDN:AAA37904.1; PID:G450452

C;Genetics:
A;Gene: Igh

Query Match 41.4%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVTS 6
|||
Db 3 MVTT 6

RESULT 10
S70335
endosperm protein, 40K - rye (fragment)
C;Species: Secale cereale (rye)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C;Accession: S70335
R;Rocher, A.; Calero, M.; Soriano, F.; Mendez, E.
Biochim. Biophys. Acta 1295, 13-22, 1996
A;Title: Identification of major rye secalins as coeliac immunoreactive proteins.
A;Reference number: S70327; MUID:96283789; PMID:8679669
A;Accession: S70335
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <ROC>

Query Match 37.9%; Score 11; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVL 3
|||
Db 1 IVL 3

RESULT 11
A27897
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - Aspergillus phoenicis (fragment)
N;Alternate names: glucoamylase
C;Species: Aspergillus phoenicis
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 06-Dec-1996
C;Accession: A27897
R;Inokuchi, N.; Takahashi, T.; Irie, M.
J. Biochem. 90, 1055-1067, 1981
A;Title: Purification and characterization of a minor glucoamylase from Aspergillus saitoi
A;Reference number: A27897; MUID:82075730; PMID:6796572
A;Note: Aspergillus saitoi
A;Accession: A27897
A;Molecule type: protein
A;Residues: 1-4 <INO>
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 34.5%; Score 10; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLV 4
|||
Db 2 VIV 4

RESULT 12
A40135
branched-chain-amino-acid transaminase (EC 2.6.1.42), mitochondrial - rat (fragment)
N;Alternate names: branched-chain-amino-acid aminotransferase, mitochondrial
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 30-Sep-1993
C;Accession: A40135
R;Hutson, S.M.; Wallin, R.; Hall, T.R.
submitted to the Protein Sequence Database, March 1992
A;Reference number: A40135
A;Accession: A40135

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <HUT>
C;Keywords: aminotransferase; mitochondrion

Query Match 34.5%; Score 10; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VTSS 7
|:|:
Db 1 VSSN 4

RESULT 13

B31836
20K protein - Rickettsia rickettsii (fragment)
C;Species: Rickettsia rickettsii
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999
C;Accession: B31836
R;Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.
J. Bacteriol. 170, 4493-4500, 1988
A;Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii
A;Reference number: A91885; MUID:89008059; PMID:3139629
A;Accession: B31836
A;Molecule type: DNA
A;Residues: 1-5 <AND>
A;Cross-references: GB:J03371; NID:G152455; PIDN:AAD15030.1; PID:G4262874

Query Match 34.5%; Score 10; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TSS 7
|:|:
Db 3 TNS 5

RESULT 14

E42364
flagellar protein flhR - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 09-Jul-2004
C;Accession: E42364
R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
J. Bacteriol. 173, 3564-3572, 1991
A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and secretion
A;Reference number: A42364; MUID:91258342; PMID:1646201
A;Accession: E42364
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5 <VOG>
A;Cross-references: UNIPROT:P26416; GB:M62408

Query Match 34.5%; Score 10; DB 2; Length 5;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVT 5
|:|:
Db 1 MIT 3

RESULT 15

PQ0728
unidentified 5.0/16K protein [imported] - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: PQ0728
R;Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A;Title: A rice protein library; a data-file of rice proteins separated by two-dimensional gel electrophoresis
A;Reference number: PQ0696

A;Accession: PQ0728
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <KOW>

Query Match 34.5%; Score 10; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVLV 4
|:|:
Db 3 IXLV 6

Search completed: August 3, 2005, 11:42:32
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:27 ; Search time 88.6667 Seconds
(without alignments)
40.427 Million cell updates/sec

Title: US-09-910-582B-4
Perfect score: 29
Sequence: 1 VVLVTSS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 174

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	44.8	7	1 CCF1_ENTFA	P20104 enterococcu
2	13	44.8	7	2 P70804	P70804 azotobacter
3	13	44.8	7	2 P72081	P72081 nocardia la
4	12	41.4	7	2 Q54248	Q54248 streptomyce
5	11	37.9	7	2 O42564	O42564 fugu rubrip
6	10	34.5	7	1 CIA_ENTFA	P11932 enterococcu
7	10	34.5	7	1 GPRF_MOUSE	P99025 mus musculu
8	9	31.0	4	1 YLM1_YEAST	P36515 saccharomyc
9	9	31.0	7	1 IGAO_DACDE	P06294 dactylium d
10	9	31.0	7	2 P83492	P83492 bionectria
11	9	31.0	7	2 P82445	P82445 nicotiana t
12	9	31.0	7	2 Q9C5B3	Q9C5B3 arabidopsis
13	9	31.0	7	2 P83530	P83530 lactobacill
14	8	27.6	4	1 ILME_SEPOF	P83568 sepiia offic
15	8	27.6	4	2 Q08433	Q08433 rattus sp.
16	8	27.6	5	1 BIOB_CITFR	P12997 citrobacter
17	8	27.6	5	1 EI04_LITRU	P82100 litoria rub
18	8	27.6	6	1 ACPH_RABIT	P25154 oryctolagus
19	8	27.6	6	1 LOKJ_LOCOMI	P41491 locusta mig
20	8	27.6	6	2 P82541	P82541 spinacia ol
21	8	27.6	7	2 P93233	P93233 lycopersico
22	8	27.6	7	2 O07354	O07354 synecococc
23	8	27.6	7	2 Q47029	Q47029 enterobacte
24	8	27.6	7	2 Q65578	Q65578 bovine herp
25	8	27.6	7	2 Q8JES1	Q8JES1 human immun
26	7	24.1	5	1 BIOA_CITFR	P13071 citrobacter
27	7	24.1	5	1 PRCT_CARMA	P67857 carcinus ma
28	7	24.1	5	1 PRCT_LIMPO	P67858 limulus pol
29	7	24.1	5	1 PRCT_PERAM	P67859 periplaneta
30	7	24.1	7	2 Q15897	Q15897 homo sapien
31	7	24.1	7	2 Q99182	Q99182 gnatholebia

P02731	homo sapien
P58261	daucus caro
P41495	sarcophaga
P81351	clostridium
P23210	human herpe
P83533	lactobacill
P80630	zea mays (m
Q8mfy6	taraxacum (
O34028	sphingomona
Q8kms3	klebsiella
Q47505	escherichia
Q8g100	borrelia bu
Q8g104	borrelia bu
Q66205	transmissib
P01858	homo sapien
P84182	eisenia foe
P82072	litorea rub
P82073	litorea rub
P83073	bacillus ce
P13736	mytilus edu
P13737	mytilus edu
P82181	spinacia ol
P82182	spinacia ol
P10420	mytilus edu
P81238	haemochus
P41874	panagrellus
P83379	lycopersico
P56576	rattus norv
Q8taq4	homo sapien
Q8g112	borrelia bu
Q67113	influenza a
Q9yq10	transmissib
P42562	hirudo medi
P42561	hirudo medi
P58707	anthopleura
P58649	octopus min
P81817	carcinus ma
P82059	litorea rub
P83308	gallus gall
P81826	juniperus v
P82070	litorea rub
P54714	canis famil
P80628	zea mays (m
P38005	chlamydia t
P82096	litorea rub
P83569	sepiia offic
P16414	pseudomonas
P81805	carcinus ma
P81806	carcinus ma
P81807	carcinus ma
P81808	carcinus ma
P82158	cydia pomon
P16101	alcaligenes
P67879	ascaris suu
P67880	panagrellus
P41871	helisoma tr
P83274	macrobrachi
P38499	procamburus
P38498	procamburus
P01153	sus scrofa
P36960	carnobacter
P42984	leptinotars
P83455	pachymedusa
P38641	mus musculu
P81675	pinus pinas
P35919	achatina fu
P35920	achatina fu
Q8nhh7	homo sapien

ALIGNMENTS

RESULT 1
CCFL_ENTFA STANDARD; PRT; 7 AA.
ID P20104;
AC 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sex pheromone cCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE
RX MEDLINE=89008313; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Adait J.C., Dunny G.M., Suzuki A.;
RT "Structure of cCF10, a peptide sex pheromone which induces conjugative
RT transfer of the Streptococcus faecalis tetracycline resistance
RT plasmid, pCF10.";
RL J. Biol. Chem. 263:14574-14578(1988).
CC -!- FUNCTION: cCF10 is involved in the conjugative transfer of the
CC hemolysin plasmid pCF10.
DR PIR; A30812; A30812.
KW Direct protein sequencing; Pheromone.
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;
Query Match 44.8%; Score 13; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 LVT 5
Db 1 LVT 3

RESULT 2
P70804 PRELIMINARY; PRT; 7 AA.
ID P70804;
AC 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Algt protein (fragment).
GN Name=algt;
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E;
RX MEDLINE=96427318; PubMed=8830682;
RA Rehm B.H.A., Estesvag H., Valla S.;
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is
RT part of an alg gene cluster physically organized in a manner similar
RT to that in Pseudomonas aeruginosa.";
RL J. Bacteriol. 178:5884-5889(1996).
DR EMBL; X87973; CAA61230.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;
Query Match 44.8%; Score 13; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 VTSS 7
Db 3 VSSS 6

RESULT 3
P72081 PRELIMINARY; PRT; 7 AA.
ID P72081;
AC 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE 3'-methylcephem hydroxylase (Fragment).
GN Name=cefF;
OS Nocardia lactamdurans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardineae; Pseudonocardaceae; Amycolatopsis.
OX NCBI_TaxID=1913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96009872; PubMed=7557411; DOI=10.1016/0378-1119(95)00308-S;
RA Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
RA Liras P.;
RT "Characterization of the cmcH genes of Nocardia lactamdurans and
RT Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem
RT O-carbamoyltransferase for cephamycin biosynthesis.";
RL Gene 162:21-27(1995).
DR EMBL; Z21682; CAA79797.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 746 MW; 75A1B2CDD1B681C0 CRC64;
Query Match 44.8%; Score 13; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 VTS 6
Db 5 VTS 7

RESULT 4
Q54248 PRELIMINARY; PRT; 7 AA.
ID Q54248;
AC 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE RplO protein (Fragment).
GN Name=rplO;
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2-3-11;
RX MEDLINE=20011291; PubMed=10542330;
RA Poehling S., Piepersberg W., Wehmeier U.F.;
RT "Analysis and regulation of the sec Y gene from Streptomyces griseus
RT N2-3-11 and interaction of the sec Y protein with the SecA protein.";
RL Biochim. Biophys. Acta 1447:298-302(1999).
DR EMBL; X95915; CAA65160.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;
Query Match 41.4%; Score 12; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 VLVT 5
Db 1 VTVT 4

RESULT 5
O42564 PRELIMINARY; PRT; 7 AA.
ID O42564;
AC O42564;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)

```

DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
DN Name=Gchfr; Synonyms=Gfrp;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RN SEQUENCE.
RC TISSUE=Liver;
RC Sanchez J.-C., Rouge V., Prutiger S., Hughes G., Yan J.X.,
RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F., Cowthorne M.;
RA Submitted (AUG-1998) to Swiss-Prot.
RL
CC -!- FUNCTION: Mediates tetrahydrobiopterin inhibition of GTP
CC cyclohydrolase I. This inhibition is reversed by L-phenylalanine
CC (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC SWISS-2DPAGE; P99025; MOUSE.
DR Direct protein sequencing.
KW INIT MET 0 0
FT NON TER 7 7
FT SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;

SQ
Query Match 34.5%; Score 10; DB 1; Length 7;
Best Local Similarity 20.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps

QY 2 VLVT5 6
DB 3 LLIST 7

RESULT 8
YLMI YEAST
ID YLMI YEAST STANDARD; PRT; 4 AA.
AC P365I5;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DT MITOCHONDRIAL 60S ribosomal protein L1 (Yml1) (Fragment).
DN Name=Yml1;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OC NCBI_TaxID=4932;
RN [1]
RN SEQUENCE.
RP MEDLINE=91285106; PubMed=2060626; DOI=10.1016/0014-5793(91)80759-V;
RX Grohmann L., Graack H.-R., Kruft V., Choll T., Goldschmidt-Reisin S.,
RX Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria.";
RT FEBS Lett. 284:51-56(1991).
CC -!- FUNCTION: Putative component of the large subunit of mitochondrial
CC ribosome.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC PIR; S17255; S17255.
KW Direct protein sequencing; Mitochondrion; Ribosomal protein.
FT NON TER 4 4
FT SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

SQ
Query Match 31.0%; Score 9; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 4 VT 5
DB 2 VT 3

RESULT 9
IGAO DACDE
ID IGAO DACDE STANDARD; PRT; 7 AA.

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AC P06294;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Galactose oxidase inhibitor.
 OS Dactylium dendroides (Glabobotryum dendroides).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.
 OX NCBI_TaxID=5132;
 RN [1]
 RP SEQUENCE.
 RA Avigad G., Markus Z.;
 RT "Identification of a peptide inhibitor of galactose oxidase from
 Dactylium dendroides.";
 RL Fed. Proc. 31:447-447(1972).
 CC -1- FUNCTION: Binds one copper ion per molecule but does not bind the
 CC galactose oxidase apoenzyme. It may inactivate the enzyme by
 CC binding to its prosthetic copper group.
 DR PIR; A01341; XEYDGD.
 KW Copper; Direct protein sequencing; Metalloenzyme inhibitor.
 SQ SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;
 QY Query Match 31.0%; Score 9; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 TSS 7
 DB 5 TES 7

RESULT 10
 P83492 ID P83492 PRELIMINARY; PRT; 7 AA.
 AC P83492;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alkaline protease Gr3 (EC 3.4.21.-) (Fragment).
 OS Bionectria ochroleuca (Gliocladium roseum).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.
 OX NCBI_TaxID=29856;
 RN [1]
 RP SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.
 RC STRAIN=Gr87;
 RA Zhao M., Zhang K.;
 RL Submitted (DCC-2002) to Swiss-Prot.
 CC -1- FUNCTION: Acts as a serine protease.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
 DR InterPro; IPR00209; Pept S8 S53.
 DR PROSITE; PS00136; SUBTILASE_ASP; PARTIAL.
 DR PROSITE; PS00137; SUBTILASE_HIS; PARTIAL.
 DR PROSITE; PS00138; SUBTILASE_SER; PARTIAL.
 KW Hydrolase; Serine protease.
 FT NON TER 7
 SQ SEQUENCE 7 AA; 688 MW; 776DD455A6C1ADB0 CRC64;
 QY Query Match 31.0%; Score 9; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 TSS 7
 DB 2 TQS 4

RESULT 11
 P82445 ID P82445 PRELIMINARY; PRT; 7 AA.
 AC P82445;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 10 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RA STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture.";
 RL Planta 0:0-0(2000).
 CC -1- SUBCELLULAR LOCATION: CELL WALL.
 CC -1- TISSUE SPECIFICITY: XYLEM.
 DR GO; GO:0005618; C:cell wall; IEA.
 KW Cell wall.
 FT NON TER 7
 SQ SEQUENCE 7 AA; 758 MW; 69D2C1E862D1B2A0 CRC64;
 QY Query Match 31.0%; Score 9; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VT 5
 DB 1 VT 2

RESULT 12
 Q9C5B3 ID Q9C5B3 PRELIMINARY; PRT; 7 AA.
 AC Q9C5B3;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein DiDi 10A-2b (Fragment).
 GN Name=DiDi 10A-2b;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Roots;
 RX MEDLINE=21171025; PubMed=11277426;
 RA Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;
 RT "Arabidopsis thaliana genes expressed in the early compatible
 RT interaction with root-knot nematodes.";
 RL Mol. Plant Microbe Interact. 14:288-299(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Roots;
 RA Vercauteren I.J.R.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ286350; CAB71014.2; -.
 KW Hypothetical protein.
 FT NON TER 1
 FT NON TER 7
 SQ SEQUENCE 7 AA; 719 MW; 6732C7287EB325D0 CRC64;
 QY Query Match 31.0%; Score 9; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVL 3
 DB 1 VVL 3

Db 5 LVL 7

RESULT 13

P83530 ID P83530 PRELIMINARY; PRT; 7 AA.

AC P83530; (T-EMBLrel. 24, Created)

DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE Unknown protein from 2D-page (Fragment).

OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).

OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;

OC Lactobacillus.

OX NCBI_TaxID=1625;

RN [1]

RP SEQUENCE.

RC STRAIN=DSM 20451;

RX PubMed=12112860;

RX DOI=10.1002/1615-9861(200206)2:6<765::AID-PROT765>3.0.CO;2-V;

RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Georg A.;

RT "High pressure effects step-wise altered protein expression in Lactobacillus sanfranciscensis.";

RL Proteomics 2:765-774(2002).

CC -1- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown protein is: 15 kDa.

FT NON TER 1 1

FT NON TER 7 7

SQ SEQUENCE 7 AA; 790 MW; 6AAB02CAA731B2A0 CRC64;

Query Match 31.0%; Score 9; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VT 5

Db 1 VT 2

RESULT 14

ILME SEPOF STANDARD; PRT; 4 AA.

AC P83568;

DT 29-MAR-2004 (Rel. 43, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Pheromone peptide ILME.

OS Sepia officinalis (Common cuttlefish).

OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;

OC Decapodiformes; Sepioidea; Sepiidae; Sepia.

OX NCBI_TaxID=6610;

RN [1]

RP SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.

RC TISSUE=Egg;

RX MEDLINE=20403899; PubMed=10944467; DOI=10.1006/bbrc.2000.3286;

RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;

RT "ILME: a waterborne pheromonal peptide released by the eggs of Sepia officinalis.";

RL Biochem. Biophys. Res. Commun. 275:217-222(2000).

RN [2]

RP SEQUENCE.

RC TISSUE=Egg;

RX MEDLINE=22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;

RA Zatylny C., Marvin L., Gagnon J., Henry J.;

RT "Fertilization in Sepia officinalis: the first mollusk sperm-attracting peptide.";

RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).

CC -1- FUNCTION: Has myotropic activity targeting the genital tract.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Follicle, fully grown oocyte and egg(EC2).

CC -1- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI; RANGES=1-4; NOTE=Ref.1. Direct protein sequencing; Pheromone.

KW

SQ SEQUENCE 4 AA; 505 MW; 6B169720300000000 CRC64;

Query Match 27.6%; Score 8; DB 1; Length 4;

Best Local Similarity 33.3%; Pred. No. 1.6e+06;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLV 4

Db 1 ILM 3

RESULT 15

Q08433 ID Q08433 PRELIMINARY; PRT; 4 AA.

AC Q08433;

DT 01-NOV-1996 (T-EMBLrel. 01, Created)

DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE Bilirubin UDP-glucuronosyltransferase (Fragment).

OS Rattus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10118;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Gunn;

RX MEDLINE=91282758; PubMed=1840486;

RA Sato H., Aono S., Kashiwamata S., Koiwai O.;

RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the hyperbilirubinemic Gunn rat.";

RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).

DR EMBL; S38636; AAB19259.1; -

DR GO; GO:0016740; F:transferase activity; IEA.

KW Transferase.

FT NON TER 4 4

SQ SEQUENCE 4 AA; 473 MW; 633732C4200000000 CRC64;

Query Match 27.6%; Score 8; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VL 3

Db 2 VL 3

Search completed: August 3, 2005, 12:07:39

Job time : 88.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:27 ; Search time 96.3333 Seconds
(without alignments)
28.104 Million cell updates/sec

Title: US-09-910-582B-4

Perfect score: 29

Sequence: 1 VVLVTSS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 121728

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	7	4	AAB30897 Peptide w
2	29	100.0	7	4	AAB50799 Heart hom
3	19	65.5	6	2	AAB31141 Anti-meli
4	19	65.5	7	7	ADE39237 Oestrogen
5	18	62.1	5	7	ADC55448 Epimorphi
6	18	62.1	6	7	ADC55447 Epimorphi
7	18	62.1	7	3	AAV15720 Peptide u
8	18	62.1	7	3	AAV80874 Fluoropho
9	18	62.1	7	7	ADC55446 Epimorphi
10	17	58.6	4	2	AAR34100 Peptide w
11	17	58.6	4	2	AAR34038 Peptide w
12	17	58.6	4	2	AAR34090 Peptide w
13	17	58.6	5	3	AAB16520 Angiogene
14	17	58.6	5	5	AAM48891 Fibrinoge
15	17	58.6	5	7	ADD12160 Tumour su
16	17	58.6	6	2	AAR34098 Antigen t
17	17	58.6	6	2	AAR34036 Antigen t
18	17	58.6	6	2	AAR34088 Antigen t
19	17	58.6	6	2	AAW25205 VTL-Pepti
20	17	58.6	6	2	AAW43157 Anti-meli
21	17	58.6	6	5	ABG35151 Ovarian c
22	17	58.6	6	5	ABG60399 Selective
23	17	58.6	6	7	ADD12161 Tumour su
24	17	58.6	7	2	AAR44042 Agarase e
25	17	58.6	7	2	AAR88312 Beta-agar

26	17	58.6	7	2	AAW73145	Beta-agar
27	17	58.6	7	5	ABG96763	Human leu
28	17	58.6	7	7	ADD12162	Tumour su
29	17	58.6	7	7	ADL98580	Human leu
30	17	58.6	7	8	ADI138690	Cancer va
31	16	55.2	5	2	AAR12433	Protease
32	16	55.2	5	8	ADR28814	Immunosup
33	16	55.2	6	2	AAR05972	Somatic i
34	16	55.2	6	2	AAW43142	Anti-meli
35	16	55.2	6	2	AAW43135	Anti-meli
36	16	55.2	6	2	AAW43134	Anti-meli
37	16	55.2	6	4	AAB48417	Human ICA
38	16	55.2	6	5	ABB90504	Hominidae
39	16	55.2	6	7	ABM74170	DNA clone
40	16	55.2	7	2	AAR26350	Fungicida
41	16	55.2	7	2	AAR90626	S. solfat
42	16	55.2	7	2	AAW25759	PHA depol
43	16	55.2	7	2	AAW25759	PHA depol
44	16	55.2	7	3	AAW76119	Membrane
45	16	55.2	7	3	AAW90823	Murine sk
46	16	55.2	7	4	AAB56058	Skin cell
47	16	55.2	7	4	AAB81547	Zif268 zi
48	16	55.2	7	5	ABB72258	Murine pe
49	16	55.2	7	6	ABP58769	Peptide c
50	16	55.2	7	7	ADA07589	Human sec
51	16	55.2	7	8	ADJ87953	Bioactive
52	16	55.2	7	8	ADN41515	Novel hum
53	15	51.7	5	5	ABB99064	N-termina
54	15	51.7	5	5	AAU85442	Human col
55	15	51.7	5	6	ABP70390	Tryptic p
56	15	51.7	5	8	ADI00219	Endopin-2
57	15	51.7	5	8	ADI00220	Endopin-2
58	15	51.7	6	2	AAR57003	N-termina
59	15	51.7	6	2	AAR85518	Anti-meli
60	15	51.7	6	2	AAW08672	Honeybee
61	15	51.7	6	2	AAW08699	Honeybee
62	15	51.7	6	2	AAW43136	Anti-meli
63	15	51.7	6	2	AAW43138	Anti-meli
64	15	51.7	6	2	AAW43129	Anti-meli
65	15	51.7	6	2	AAW43140	Anti-meli
66	15	51.7	6	2	AAW43143	Anti-meli
67	15	51.7	6	2	AAW43130	Anti-meli
68	15	51.7	6	2	AAW43139	Anti-meli
69	15	51.7	6	2	AAW43144	Peptide #
70	15	51.7	6	2	AAW43131	Anti-meli
71	15	51.7	6	2	AAW43137	Anti-meli
72	15	51.7	6	2	AAW43132	Anti-meli
73	15	51.7	6	2	AAW43146	Peptide #
74	15	51.7	6	2	AAW43117	Anti-meli
75	15	51.7	6	2	AAW43147	Peptide #
76	15	51.7	6	2	AAW43143	Anti-meli
77	15	51.7	6	2	AAW43145	Peptide #
78	15	51.7	6	3	AAV50659	Alphai-pr
79	15	51.7	6	3	AAV91891	Peptide 6
80	15	51.7	6	5	AAU78502	Gamma sec
81	15	51.7	6	5	ABB08057	Human pce
82	15	51.7	6	5	ABG98337	Secreted
83	15	51.7	6	8	ADN65991	Human 273
84	15	51.7	6	8	ADN05582	Antipsori
85	15	51.7	6	8	ADO04697	Human int
86	15	51.7	7	2	AAR26356	Fungicida
87	15	51.7	7	2	AAR26357	Fungicida
88	15	51.7	7	2	AAR26354	Fungicida
89	15	51.7	7	2	AAR26353	Fungicida
90	15	51.7	7	2	AAR26349	Fungicida
91	15	51.7	7	5	ABB83038	Transferr
92	15	51.7	7	5	ABG77666	Targettin
93	15	51.7	7	7	ADB79562	Parapoxvi
94	15	51.7	7	7	ADB33536	APP gamma
95	15	51.7	7	7	ADG64518	Family A
96	15	51.7	7	7	ADG64331	Thermosta
97	15	51.7	7	8	ADH96974	S. pneumo
98	15	51.7	7	8	ADK72039	Antimicro

99 15 51.7 7 8 ADP74973 Parapoxvi
100 15 51.7 7 8 ADR72658 Human mon

ALIGNMENTS

RESULT 1
AAB30897
ID AAB30897 standard; peptide; 7 AA.
XX AC
XX AAB30897;
XX DT 02-APR-2001 (first entry)
XX DE Peptide which selectively binds to normal cardiac endothelium.
XX KW Cardiac endothelium; angiogenic factor; vascular endothelium;
XX KW peripheral vascular disease; cardiovascular disease; angiogenesis;
XX KW cardiac neovascularisation.
XX OS Unidentified.

XX WO200075329-A1.
XX PD 14-DEC-2000.
XX PF 31-MAY-2000; 2000WO-US014988.
XX PR 07-JUN-1999; 99US-00327045.
XX PA (EDWA-) EDWARDS LIFESCIENCES CORP.
XX PA (BAXT) BAXTER AG.
XX PI Levine AJ, Mitterer A, Falkner F, Scheiflinger F, Dörner F;
XX DR WPI; 2001-091212/10.
XX XX

PT New chimeric molecules having an angiogenic factor linked to a targeting
PT molecule that binds to a vascular endothelium, useful for increasing
PT cardiac neovascularization, or treating peripheral vascular and
PT cardiovascular diseases.

PS Disclosure; Page 27; 67pp; English.

XX AAB30895-99 represent targeting molecules, which are used to produce the
CC chimeric molecules of the invention. AAB30895-98 selectively bind to
CC normal cardiac endothelium. The specification describes a chimeric
CC molecule comprising an angiogenic factor linked to a targeting molecule
CC that specifically binds to a vascular endothelium. The chimeric molecules
CC are useful for treatment of peripheral vascular or cardiovascular
CC diseases. Specifically, they are useful for inducing or inhibiting
CC angiogenesis, for increasing cardiac neovascularisation in ischemic
CC tissue in the peripheral vascular system

XX Sequence 7 AA;

Query Match 100.0%; Score 29; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVLVTSS 7
Db 1 VVLVTSS 7

RESULT 2
AAB50799
ID AAB50799 standard; peptide; 7 AA.
XX AC
XX AAB50799;
XX DT 21-MAR-2001 (first entry)

XX Heart homing peptide SEQ ID NO: 4.
DE
XX Heart homing peptide; cardiovascular disease; ischaemic disease;
KW gene therapy.
XX OS Synthetic.

XX WO200075174-A1.
XX PD 14-DEC-2000.
XX PF 31-MAY-2000; 2000WO-US015088.
XX PR 07-JUN-1999; 99US-00326718.
XX PA (BURN-) BURNHAM INST.

XX Ruoslahti E, Mackenna DA;
XX DR WPI; 2001-071059/08.
XX PT

Novel heart homing peptide that selectively homes to normal ischemic and
cardiac tissue useful for targeting ischemic tissues for treating
ischemic and cardiovascular diseases such as atherosclerosis and
restenosis.

Claim 2; Page 55; 70pp; English.

XX The present invention provides a number of heart homing peptides which
CC selectively home to cardiac tissue. These can be used in the treatment of
CC cardiovascular and ischaemic diseases, such as atherosclerosis, myocardial
CC thrombosis, restenosis, vasculitis, atherosclerotic aneurysms, myocardial
CC hypertrophy, congenital heart diseases, ischaemic heart disease and
CC anginas, acquired valvular/endocardial diseases, primary myocardial
CC diseases, cardiac tumours and arrhythmias

XX Sequence 7 AA;

Query Match 100.0%; Score 29; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVLVTSS 7
Db 1 VVLVTSS 7

RESULT 3
AAW43141
ID AAW43141 standard; peptide; 6 AA.

XX AAW43141;

XX 31-MAR-1998 (first entry)

XX Anti-melittin peptide #20.

XX Anti-melittin peptide; bee sting; melittin; haemolytic activity;
KW bee venom; red blood cell; cell lysis; anti-microbial.

XX Synthetic.

XX Key Location/Qualifiers
XX Modified-site 1 /note= "N-terminally acetylated"
XX Modified-site 6 /note= "C-terminally amidated"

XX US5698673-A.
XX 16-DEC-1997.
XX

PF 04-MAY-1995; 95US-00434761.
 XX 18-JUN-1993; 93US-00079445.
 XX (TORR-) TORREY PINES INST.
 XX Houghten RA, Pinilla C, Blondelle SE;
 XX WPI; 1998-051545/05.
 XX Anti-mellitin peptide(s) - useful for treating bee stings.
 XX Example 2; Col 32; 26pp; English.
 XX This sequence represents a specific example of a peptide having anti-mellitin activity with an IC50 value of less than 30 microg/ml. It is useful for treating mellitin poisoning. Mellitin is the active compound in bee venom and causes cell lysis. Peptides having anti-mellitin activity have one of the following formulae; Ac-IVILIZZ-NH2; Ac-IVILTZ-NH2; Ac-IVILIZ-NH2; Ac-IVIPFZ-NH2; Ac-Z1-Z2-I-Z3-Z4-E-NH2; Ac-MILWIE-NH2; Ac-VIOQFV-NH2; Ac-WIQIFI-NH2; where Z= an optionally methylated or chlorinated D-form or natural amino acid; Z1= F or I; Z2= I or Q; Z3= W or Y and Z4= C or F
 XX Sequence 6 AA;
 Query Match 65.5%; Score 19; DB 2; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VLVITS 6
 Db 1 IVILTS 6
 RESULT 4
 ADE39237
 ID ADE39237 standard; peptide; 7 AA.
 XX ADE39237;
 XX 29-JAN-2004 (first entry)
 XX Oestrogen receptor-alpha specific monobody peptide seq id 35.
 XX nuclear receptor antagonist; nuclear receptor agonist;
 KW fibronectin type III; Fn3; polypeptide monobody;
 KW nuclear receptor binding activity; drug screening;
 KW protein activity modulator; lexA; oestrogen receptor alpha; ER-alpha; monobody; motif.
 XX Synthetic.
 XX US2003186385-A1.
 XX 02-OCT-2003.
 XX 19-NOV-2001; 2001US-00006760.
 XX 17-NOV-2000; 2000US-0249756P.
 XX (KOID/) KOIDE S.
 XX Koide S;
 XX WPI; 2003-803152/75.
 XX New fibronectin type III polypeptide monobody useful for screening a candidate drug for nuclear receptor agonist or antagonist activity, and to validate target protein activity.
 XX Example 2; SEQ ID NO 35; 45pp; English.

CC The invention describes a fibronectin type III (Fn3) polypeptide monobody (I) comprising 2 Fn3 beta-strand domain sequences with a loop region sequence linked between adjacent beta-strand domain sequences; and optionally an N-terminal tail of 2 amino acids, a C-terminal tail of 2 amino acids, or both. The loop region sequence, N-terminal tail, or C-terminal tail comprises an amino acid sequence which varies by deletion, insertion, or replacement of 2 amino acids from the corresponding region in a wild-type Fn3 domain of fibronectin, and the monobody exhibits nuclear receptor binding activity. (I) is used to screen a candidate drug for nuclear receptor agonist or antagonist activity, and is used to validate target protein activity. (I) is also used to measure the binding affinity of (I) for a target protein, and can modulate target protein activity. A new method is used to identify (I). (I) can also be used in therapeutics. This is the amino acid sequence of a motif occurring in monobodies selected in the presence of an agonist while using the LexA-oestrogen receptor alpha fusion protein as prey in a two-hybrid assay.
 XX Sequence 7 AA;
 Query Match 65.5%; Score 19; DB 7; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 VLVTS 7
 Db 2 VLITRS 7
 RESULT 5
 ADC55448
 ID ADC55448 standard; peptide; 5 AA.
 XX ADC55448;
 XX 18-DEC-2003 (first entry)
 XX Epimorphin activity control oligopeptide #3.
 XX oligopeptide; epimorphin.
 XX Unidentified.
 XX JP2003146998-A.
 XX 21-MAY-2003.
 XX 13-NOV-2001; 2001JP-00347339.
 XX 13-NOV-2001; 2001JP-00347339.
 XX (SUME) SUMITOMO ELECTRIC IND LTD.
 XX WPI; 2003-818309/77.
 XX Novel oligopeptide possessing binding capacity to epimorphin and controlling activity of epimorphin, useful as hair growth retardant and hair growth stimulant.
 XX Claim 1; SEQ ID NO 3; 11pp; Japanese.
 XX The present invention relates to an oligopeptide possessing binding capacity to epimorphin, controlling activity of epimorphin. The present sequence is contained in the epimorphin activity control oligopeptide of the invention.
 XX Sequence 5 AA;
 Query Match 62.1%; Score 18; DB 7; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 LVTS 7
 Db 3 LVTS 7

```

Db      1 LLTSS 5

RESULT 6
ID      ADC55447
AC      ADC55447 standard; peptide; 6 AA.
XX
XX
XX      18-DEC-2003 (first entry)
XX      Epimorphin activity control oligopeptide #2.
XX
XX      oligopeptide; epimorphin.
XX
XX      Unidentified.
XX
XX      JP2003146998-A.
XX
XX      21-MAY-2003.
XX
XX      13-NOV-2001; 2001JP-00347339.
XX
XX      13-NOV-2001; 2001JP-00347339.
XX      (SUME ) SUMITOMO ELECTRIC IND LTD.
XX
XX      WPI; 2003-818309/77.
XX
XX      Novel oligopeptide possessing binding capacity to epimorphin and
XX      controlling activity of epimorphin, useful as hair growth retardant and
XX      hair growth stimulant.
XX
XX      Claim 2; SEQ ID NO 2; 11pp; Japanese.
XX
XX      The present invention relates to an oligopeptide possessing binding
XX      capacity to epimorphin, controlling activity of epimorphin. The present
XX      sequence is contained in the epimorphin activity control oligopeptide of
XX      the invention.
XX
XX      Sequence 6 AA;

Query Match      62.1%; Score 18; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 LVTSS 7
       |:|:|
Db      1 LLTSS 5

RESULT 7
AAY15720
ID      AAY15720 standard; peptide; 7 AA.
XX
XX      AAY15720;
XX
XX      27-JUL-1999 (first entry)
XX
XX      Peptide used to make fluorescent reporter molecules.
XX
XX      Fluorogenic; fluorescent reporter molecule; enzyme substrate; apoptosis;
XX      protease; peptidase; apoptosis cascade; cancer; chemotherapeutic agent;
XX      cell death; viral protease activity.
XX
XX      Synthetic.
XX
XX      WO9918856-A1.
XX
XX      22-APR-1999.
XX
XX      09-OCT-1998; 98WO-US021231.
XX

Query Match      62.1%; Score 18; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 LVTSS 7
       |:|:|
Db      1 LLTSS 5

RESULT 7
AAY15720
ID      AAY15720 standard; peptide; 7 AA.
XX
XX      AAY15720;
XX
XX      27-JUL-1999 (first entry)
XX
XX      Peptide used to make fluorescent reporter molecules.
XX
XX      Fluorogenic; fluorescent reporter molecule; enzyme substrate; apoptosis;
XX      protease; peptidase; apoptosis cascade; cancer; chemotherapeutic agent;
XX      cell death; viral protease activity.
XX
XX      Synthetic.
XX
XX      WO9918856-A1.
XX
XX      22-APR-1999.
XX
XX      09-OCT-1998; 98WO-US021231.
XX

Query Match      62.1%; Score 18; DB 2; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 VLVLTSS 7
       |:|:|
Db      1 LVLASSS 7

RESULT 8
AAY80874
ID      AAY80874 standard; peptide; 7 AA.
XX
XX      AAY80874;
XX
XX      22-MAY-2000 (first entry)
XX
XX      Fluorophore-labelled protease substrate peptide, SEQ ID NO:103.
XX
XX      Protease substrate; fluorescent label; fluorophore; rhodamine;
XX      blocking group; halobenzoyle group; cleavage; caspase; viral protease;
XX      methionine aminopeptidase type 2; MetAP-2; drug screening.
XX
XX      Synthetic.
XX
XX      WO200004914-A1.
XX
XX      03-FEB-2000.
XX
XX      21-JUL-1999; 99WO-US016423.
XX
XX      21-JUL-1998; 98US-0093642P.
XX
XX      (CYTO-) CYTOVIA INC.
XX      (ZHAN/) ZHANG H.
XX      (CAIS/) CAI S X.
XX      (DREW/) DREWE J A.
XX      (YANG/) YANG W.
XX
XX      Zhang H, Cai SX, Drewe JA, Yang W;
PI

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PR      10-OCT-1997; 97US-0061582P.
PR      03-MAR-1998; 98US-00033661.
XX
XX      (CYTO-) CYTOVIA INC.
XX
XX      Weber E, Cai SX, Keana JFW, Drewe JA, Zhang H;
XX
XX      WPI; 1999-312448/26.
XX
XX      New fluorogenic or fluorescent reporter molecules.
XX
XX      Disclosure; Page 187; 202pp; English.
XX
XX      AAY15618-Y15759 represent peptides used to make the fluorogenic or
XX      fluorescent reporter molecules of the invention. These molecules contain
XX      a peptide moiety (e.g. present sequence) which acts as a substrate for
XX      enzymes involved in apoptosis or protease or peptidase enzymes. The
XX      compounds can be used as fluorogenic or fluorescent substrates for
XX      enzymes. Depending on the peptide moiety used, the fluorescent molecules
XX      can be used for detecting or measuring the activity of an enzyme involved
XX      in the apoptosis cascade in cells; to determine whether a test compound
XX      has an effect on an enzyme involved in the apoptosis cascade in cells;
XX      for determining the sensitivity of an animal with cancer to treatment
XX      with chemotherapeutic agents or determining whether a test substance
XX      inhibits, prevents, causes or enhances cell death of test cells; for
XX      detecting or measuring the activity of a viral protease in cells; for
XX      determining whether a test compound has an effect on the activity of a
XX      viral protease in cells; and for measuring the activity or determining
XX      whether a test substance has an effect on the activity of a protease or
XX      peptidase in cells
XX
XX      Sequence 7 AA;
SQ

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XX WPI; 2000-195079/17.
 XX New fluorescently labeled amino acids or peptides, used as substrates for
 PT detecting enzymes or their modulators, e.g. anticancer or antiviral
 PT agents, contains a halobenzoyl N-blocking group.
 XX Claim 33; Page 111; 174pp; English.
 XX The invention relates to fluorescently labelled peptides containing a
 CC halobenzoyl group on the fluorophore. They are of the structure peptide-Y
 CC -Z, where Z represents a halo-substituted benzoyl blocking group, Y is a
 CC fluorescent or fluorogenic moiety (preferably a rhodamine), and the
 CC peptide-Y bond is cleavable by the enzyme being assayed. The labelled
 CC peptides are reporters for detecting intracellular proteolytic enzymes,
 CC particularly caspases and other enzymes involved in apoptosis; viral
 CC proteases (e.g., HIV, herpes simplex virus-1, human cytomegalovirus and
 CC hepatitis C virus proteases); and methionine aminopeptidase type 2 (MetAP
 CC -2). The peptides are particularly used to identify modulators of these
 CC enzymes which may be potentially useful as agents for treating conditions
 CC such as cancer, neurodegeneration, autoimmune diseases, myocardial
 CC infarction and viral infection. Modulators identified may also be used to
 CC prolong the life of cells being cultured for recombinant protein
 CC production, or to monitor the treatment of cancer with chemotherapeutic
 CC agents. Inhibitors of MetAP-2 are potential anti- angiogenic or
 CC anticancer agents. Sequences AAY0782-Y80910 represent peptides, some of
 CC which are specifically claimed, which may be used in assay methods
 CC according to the invention
 XX Sequence 7 AA;
 SQ

Query Match 62.1%; Score 18; DB 3; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 VLVLTSS 7
 Db 1 LVLASS 7

RESULT 9
 ADC55446
 ID ADC55446 standard; peptide; 7 AA.
 XX
 AC ADC55446;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Epimorphin activity control oligopeptide #1.
 XX
 KW oligopeptide; epimorphin.
 XX
 OS Unidentified.
 XX
 PN JP2003146998-A.
 XX
 XX 21-MAY-2003.
 XX
 PF 13-NOV-2001; 2001JP-00347339.
 XX
 PR 13-NOV-2001; 2001JP-00347339.
 XX
 PA (SUME) SUMITOMO ELECTRIC IND LTD.
 XX
 XX WPI; 2003-818309/77.
 XX
 XX Novel oligopeptide possessing binding capacity to epimorphin and
 PT controlling activity of epimorphin, useful as hair growth retardant and
 PT hair growth stimulant.
 XX
 PS Claim 2; SEQ ID NO 1; 11pp; Japanese.
 XX
 XX The present invention relates to an oligopeptide possessing binding

CC capacity to epimorphin, controlling activity of epimorphin. The present
 CC sequence is contained in the epimorphin activity control oligopeptide of
 CC the invention.
 XX Sequence 7 AA;
 SQ

Query Match 62.1%; Score 18; DB 7; Length 7;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 LVTSS 7
 Db 1 LVTSS 5

RESULT 10
 AAR34100
 ID AAR34100 standard; peptide; 4 AA.
 XX
 AC AAR34100;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-AUG-1993 (first entry)
 XX
 DE Peptide which binds the ICAM-1 binding site on IRBC.
 XX
 KW Immunoadhesin; Plasmodium falciparum infected erythrocyte; CD36; malaria;
 KW intercellular adhesion molecule; ICAM-1; CD54; endothelial receptor;
 KW antibody.
 XX
 OS Homo sapiens.
 XX
 PN WO9306848-A1.
 XX
 PD 15-APR-1993.
 XX
 PF 05-OCT-1992; 92WO-US008482.
 XX
 PR 03-OCT-1991; 91US-00769625.
 PR 03-APR-1992; 92US-00862708.
 PR 12-JUN-1992; 92US-00899061.
 XX
 PA (BLOO-) CENT BLOOD RES.
 XX
 PI Staunton DE, Springer TA;
 XX
 DR WPI; 1993-134130/15.
 XX
 PT Inhibition of CD36 binding to malaria infected erythrocytes - by
 PT administering an antibody covalently attached to CD36 or CD36 fragment,
 PT useful in diagnosis or treatment of PLASMODIUM FALCIPARUM malaria.
 XX
 PS Disclosure; Page 49; 66pp; English.
 XX
 CC The peptide AAR34099 is capable of binding the ICAM-1 binding site on an
 CC IRBC. See related patents WO9306849 and WO9306850. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX
 XX Sequence 4 AA;
 SQ

Query Match 58.6%; Score 17; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 VLVLT 5
 Db 1 VLVLT 4

RESULT 11
 AAR34038
 ID AAR34038 standard; peptide; 4 AA.
 XX

AC AAR34038;
 XX
 XX 25-MAR-2003 (revised)
 DT 09-JAN-2003 (revised)
 DT 06-AUG-1993 (first entry)
 XX
 XX Peptide which binds the ICAM-1 binding site on IRBC.
 DE
 XX
 XX Immunoadhesin; Plasmodium falciparum infected erythrocyte; IRBC; malaria;
 KW intercellular adhesion molecule; ICAM-1; CD54; endothelial receptor;
 KW antibody.
 KW
 XX Unidentified.
 OS
 XX
 XX WO9306849-A1.
 PN
 XX
 XX 15-APR-1993.
 PD
 XX
 XX 05-OCT-1992; 92WO-US008483.
 XX
 XX 03-OCT-1991; 91US-00769625.
 PR
 PR 03-APR-1992; 92US-00862708.
 PR
 PR 12-JUN-1992; 92US-00899064.
 XX
 XX (BLOO-) CENT BLOOD RES.
 PA (USSA) US SEC OF ARMY.
 PA
 XX Staunton DE, Springer TA, Ockenhouse CF;
 XX
 XX WPI; 1993-134131/16.
 DR
 XX
 XX Inhibition of CD36 binding to malaria infected erythrocytes - by admin of
 PT CD36 or suitable fragment antibody etc.; useful in diagnosis and
 PT treatment of PLASMODIUM FALCIPARUM malaria.
 PT
 XX Disclosure; Page 46; 62pp; English.
 PS
 XX The peptide AAR34038 is capable of binding the ICAM-1 binding site on an
 CC IRBC. See related patents WO9306848 and WO9306850. (Updated on 09-JAN-
 CC 2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 XX Sequence 4 AA;
 SQ
 Query Match 58.6%; Score 17; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 VLVT 5
 Db 1 VLVT 4
 XX
 XX Peptide which binds the ICAM-1 binding site on IRBC.
 DE
 XX
 XX Immunoadhesin; Plasmodium falciparum infected erythrocyte; IRBC; malaria;
 KW intercellular adhesion molecule; ICAM-1; CD54; endothelial receptor;
 KW antibody.
 KW
 XX Homo sapiens.
 OS
 XX WO9306850-A1.
 PN
 XX 15-APR-1993.
 PD

XX 05-OCT-1992; 92WO-US008484.
 PF
 XX 03-OCT-1991; 91US-00769625.
 PR
 PR 03-APR-1992; 92US-00862708.
 PR
 PR 12-JUN-1992; 92US-00899063.
 XX
 XX (BLOO-) CENT BLOOD RES.
 PA (USSA) US SEC OF ARMY.
 PA
 XX Staunton DE, Springer TA, Ockenhouse CF;
 XX
 XX WPI; 1993-134132/16.
 DR
 XX
 XX Inhibition of ICAM-1 binding to malaria-infected erythrocytes - by admin.
 PT of ICAM-1 or fragment, antibody etc.; useful in diagnosis or treatment of
 PT PLASMODIUM FALCIPARUM malaria.
 PT
 XX Claim 9; Page 49; 67pp; English.
 PS
 XX The peptide AAR34090 is capable of binding the ICAM-1 binding site on an
 CC IRBC. See related patents WO9306848 and WO9306849. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 CC
 XX Sequence 4 AA;
 SQ
 Query Match 58.6%; Score 17; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 VLVT 5
 Db 1 VLVT 4
 XX
 XX RESULT 13
 AAAB16520
 ID AAB16520 standard; peptide; 5 AA.
 XX
 XX AAB16520;
 AC
 XX 27-OCT-2000 (first entry)
 DT
 XX
 XX Angiogenesis-inhibiting protein receptor peptide fragment SEQ ID # 111.
 DE
 XX Angiogenesis-inhibiting protein receptor; angiogenesis; angiostatin;
 KW endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;
 KW psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease;
 KW cerebral collateral; arteriovenous malformation; rubecosis; cancer;
 KW diabetic retinopathy; arthritis; wound healing; peptic ulcer;
 KW Helicobacter related disease; fracture; cat scratch fever.
 KW
 XX Synthetic.
 OS
 XX WO2000032631-A2.
 PN
 XX 08-JUN-2000.
 PD
 XX
 XX 06-DEC-1999; 99WO-US028897.
 PF
 XX 04-DEC-1998; 98US-00206059.
 PR
 XX (ENTR-) ENTREMED INC.
 PA
 XX Macdonald NJ, Sim KL;
 PI WPI; 2000-412290/35.
 XX
 XX New angiogenesis-inhibiting protein receptors, useful in methods for
 PT treating diseases and processes that are mediated by angiogenesis, such
 PT as solid tumors, psoriasis, scleroderma and myocardial angiogenesis.
 XX
 XX Claim 1; Page 52; 100pp; English.
 PS

XX This invention relates to angiogenesis-inhibiting protein receptors, and
 CC the DNA sequences encoding them. Angiogenesis is the generation of new
 CC blood vessels into a tissue, and normally occurs in wound healing, foetal
 CC and embryonal development and the formation of the corpus luteum,
 CC endometrium and placenta. Angiostatin is a protein (see AAB16450 and
 CC AAB68202) involved in angiogenesis, and has an amino acid sequence
 CC similar to that of a plasminogen fragment (see murine plasminogen
 CC AAB16490). Angiostatin has the ability to inhibit angiogenesis.
 CC Angiostatin is also an angiogenesis inhibiting protein (see AAB16451 and
 CC AAB68203). Sequences AAB68242 and AAB16522 represent coding and protein
 CC sequences of human laminin. Laminin is an angiostatin binding protein,
 CC and some of the peptides of the invention share homology with regions of
 CC laminin. Peptides AAB16452-B16521 (excluding AAB16490) are the
 CC angiogenesis-inhibiting protein receptor fragments of the invention. The
 CC peptides bind either angiostatin or endostatin and can be used in methods
 CC for treating diseases and processes that are mediated by angiogenesis,
 CC such as solid tumours, psoriasis, scleroderma, myocardial angiogenesis,
 CC Crohn's disease, cerebral collaterals, arteriovenous malformations,
 CC rubecosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers,
 CC Helicobacter related diseases, fractures, placental and cat scratch
 CC fever. They are useful for the detection and prognosis of cancer. DNA
 CC sequences A628204-A628241 encode the peptides of the invention
 XX

SQ Sequence 5 AA;

Query Match 58.6%; Score 17; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVTS 6
 ||||
 DB 1 LVTS 4

RESULT 14
 AAM48891
 ID AAM48891 standard; peptide; 5 AA.

XX AAM48891;

XX 04-APR-2002 (first entry)

XX Fibrinogen alpha 443 peptide fragment.

XX Human; angiostatin; endostatin; angiogenesis; cancer; metastasis;
 KW psoriasis; scleroderma; Crohn's disease; corneal disease; retinopathy;
 KW arthritis; wound healing; Helicobacter pylori; peptic ulcer;
 KW gene therapy; angiostatin antagonist; endostatin antagonist;
 KW antiangiogenic; cytostatic; antiarthritic; antiinflammatory;
 KW cerebroprotective; antidiabetic; virucide; antipyretic; vulnerary;
 KW gynaecological; cat scratch fever.

XX Unidentified.

XX WO200193897-A2.

XX 13-DEC-2001.

XX 04-JUN-2001; 2001WO-US017947.

XX 02-JUN-2000; 2000US-0209065P.

XX 08-MAY-2001; 2001US-0289387P.

XX (ENTR-) ENTREMED INC.

XX Sim KL, Macdonald NJ;

XX WPI; 2002-130569/17.

XX Regulating angiogenesis and treatment of angiogenesis-mediated diseases,
 PT e.g. hemangioma, tumors or cancer, by administering a tropomyosin binding
 PT compound or actin disrupting compound.

XX Example 11; Page 63; 95pp; English.

XX The present invention relates to methods of regulating angiogenesis in an
 CC individual by administering an angiogenesis regulating composition
 CC comprising a tropomyosin binding compound or an actin disrupting
 CC compound. The compositions are useful for treating diseases and processes
 CC mediated by angiogenesis including haemangioma, solid tumours, blood
 CC borne tumours, leukaemia, metastasis, Crohn's disease, coronary or
 CC cerebral collaterals, arthritis, diabetic neovascularisation, macular
 CC degeneration, wound healing, Helicobacter related diseases, ovulation,
 CC menstruation, and cat scratch fever. The present sequence is a peptide
 CC described in the exemplification of the invention
 XX

SQ Sequence 5 AA;

Query Match 58.6%; Score 17; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVTS 6
 ||||
 DB 1 LVTS 4

RESULT 15
 ADD12160
 ID ADD12160 standard; peptide; 5 AA.

XX ADD12160;

XX 01-JAN-2004 (first entry)

XX Tumour suppressor/cell viability/critical regulator PL peptide #463.

XX modulator; PDZ; post-synaptic density protein 95; PSD95;
 KW Drosophila large disc protein; Zonula Occludin 1 protein; ZO-1;
 KW PDZ ligand; antiinflammatory; antiallergic; antiulcer; antipsoriatic;
 KW antiasthmatic; dermatological; neuroprotective; virucide; antidiabetic;
 KW osteopathic; antiarthritic; immunosuppressive; antiatherosclerotic;
 KW cytostatic; anti-HIV; vasotropic; immunomodulator; neurological disease;
 KW immune response disease; muscular disease; cancer;
 KW modulating vesicular trafficking; tumour suppression;
 KW signal transduction; protein sorting; membrane polarity; apoptosis;
 KW synapse formation; multi-protein complex; leukocyte activation inhibitor;
 KW tumour suppressor; cell viability; critical regulator.

XX Unidentified.

XX WO2003014303-A2.

XX 20-FEB-2003.

XX 02-AUG-2002; 2002WO-US024655.

XX 03-AUG-2001; 2001US-0309841P.

XX 25-FEB-2002; 2002US-0360061P.

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS, Rabinowitz JD, Schweizer J, Carrick DM;

XX WPI; 2003-268193/26.

XX Modulator of binding between discs-large homology repeat protein, PDZ and
 PT PDZ ligand protein, is a peptide having few residues of C-terminal
 PT sequence of PDZ ligand protein.

XX Disclosure; Page 42; 172pp; English.

XX The invention relates to a novel modulator of binding between a PDZ
 CC protein (post-synaptic density protein 95 (PSD95), Drosophila large disc
 CC protein and Zonula Occludin 1 protein (ZO-1)) and a PDZ ligand (PL)

CC protein. The modulator is a peptide having 3 residues of a C-terminal
CC sequence of a PL protein. PDZ and PL proteins are a binding pair given in
CC specification, or a peptide mimetic of the 3 residue PL protein, or a
CC small molecule having similar functional activity as the 3 residue PL
CC protein. The reagents of the invention have the following activities:
CC antiinflammatory, anti-allergic, antiulcer, antipsoriatic, antiasthmatic,
CC dermatological, neuroprotective, virucide, antidiabetic, osteopathic,
CC antiarthritic, immunosuppressive, antiatherosclerotic, cytostatic, anti-
CC HIV, vasotropic, and immunomodulator. The novel modulator is useful for
CC treating a disease correlated with binding between a PDZ protein and PL
CC protein. The disease can be a neurological disease, immune response
CC disease, muscular disease or cancer. The modulator is useful for
CC modulating vesicular trafficking, tumour suppression, signal
CC transduction, protein sorting, establishment of membrane polarity,
CC apoptosis, regulation of immune response and organisation of synapse
CC formation. The modulator is useful for facilitating the assembly of multi
CC -protein complexes, often serving as a bridge between several proteins,
CC or regulating the function of other proteins, and to inhibit leukocyte
CC activation. The modulator is useful for treating diseases characterised
CC by inflammatory and humoral immune responses e.g., inflammation, allergy,
CC inflammatory bowel diseases, ulcerative colitis, psoriasis, asthma,
CC allergic rhinitis, atopic dermatitis, arthritis, multiple sclerosis,
CC diabetes, osteoarthritis, graft-versus-host diseases, atherosclerosis,
CC leukaemia, infectious diseases (viral infection such as human
CC immunodeficiency virus (HIV)), and ischaemia. This sequence represents a
CC PL protein C-terminal core peptide of a tumour suppressor, cell
CC viability, or critical regulator of the invention.

XX
SQ Sequence 5 AA;

Query Match 58.6%; Score 17; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LVTS 6
|||
Db 1 LVTS 4

Search completed: August 3, 2005, 12:03:14
Job time : 100.333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:26 ; Search time 25 Seconds
(without alignments)
20.902 Million cell updates/sec

Title: US-09-910-582B-4
Perfect score: 29
Sequence: 1 VLVLTSS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 61165

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	29	100.0	7	3	US-09-326-718-4
2	18	62.1	7	3	US-09-357-952-103
3	18	62.1	7	3	US-09-521-650-103
4	18	62.1	7	3	US-09-168-888-103
5	18	62.1	7	4	US-09-947-387-103
6	17	58.6	7	2	US-08-554-591-1
7	16	55.2	6	2	US-08-760-075A-33
8	16	55.2	6	3	US-09-338-546-33
9	16	55.2	6	4	US-09-659-084-33
10	16	55.2	7	3	US-08-840-204-4
11	16	55.2	7	3	US-09-258-754-296
12	16	55.2	7	3	US-09-960-780-75
13	16	55.2	7	3	US-09-042-107-296
14	16	55.2	7	3	US-09-073-898-75
15	16	55.2	7	3	US-09-227-357-410
16	16	55.2	7	3	US-09-298-924-14
17	16	55.2	7	4	US-09-324-494A-4
18	16	55.2	7	4	US-09-312-283C-398
19	16	55.2	7	4	US-09-722-250D-296
20	16	55.2	7	4	US-09-850-351A-75
21	16	55.2	7	4	US-09-676-475A-296
22	15	51.7	5	1	US-08-220-401-19
23	15	51.7	5	2	US-08-437-362-19
24	15	51.7	6	1	US-07-752-101A-9
25	15	51.7	6	1	US-08-079-445-9
26	15	51.7	6	1	US-08-434-761-9
27	15	51.7	6	2	US-09-127-574-39
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					Sequence 103, App
					Sequence 103, App
					Sequence 103, App
					Sequence 103, App
					Sequence 1, Appli
					Sequence 33, Appl
					Sequence 33, Appl
					Sequence 4, Appli
					Sequence 296, App
					Sequence 75, Appl
					Sequence 296, App
					Sequence 14, Appli
					Sequence 398, App
					Sequence 296, App
					Sequence 75, Appl
					Sequence 296, App
					Sequence 19, Appl
					Sequence 19, Appl
					Sequence 9, Appli
					Sequence 9, Appli
					Sequence 9, Appli
					Sequence 39, Appl

28	15	51.7	6	4	US-09-621-377B-25	Sequence 25, Appl
29	15	51.7	6	4	US-10-031-893-25	Sequence 25, Appl
30	15	51.7	7	1	US-08-191-866D-32	Sequence 32, Appl
31	15	51.7	7	2	US-08-446-345-41	Sequence 41, Appl
32	15	51.7	7	2	US-08-185-948B-32	Sequence 32, Appl
33	15	51.7	7	4	US-08-753-750B-16	Sequence 16, Appl
34	14	48.3	4	4	US-09-443-199C-1251	Sequence 1251, Ap
35	14	48.3	4	4	US-09-443-199C-1252	Sequence 1252, Ap
36	14	48.3	5	3	US-08-288-059-6	Sequence 6, Appli
37	14	48.3	5	3	US-09-339-944-4	Sequence 4, Appli
38	14	48.3	5	4	US-09-651-265-4	Sequence 4, Appli
39	14	48.3	6	1	US-07-923-260A-8	Sequence 8, Appli
40	14	48.3	6	3	US-08-134-198B-28	Sequence 28, Appl
41	14	48.3	6	3	US-08-134-198B-29	Sequence 29, Appl
42	14	48.3	6	3	US-08-134-198B-30	Sequence 30, Appl
43	14	48.3	6	3	US-09-177-249-14	Sequence 14, Appl
44	14	48.3	6	3	US-09-357-952-104	Sequence 104, App
45	14	48.3	6	3	US-09-521-650-104	Sequence 104, App
46	14	48.3	6	3	US-09-168-888-104	Sequence 104, App
47	14	48.3	6	4	US-09-155-613A-52	Sequence 52, Appl
48	14	48.3	6	4	US-09-947-387-104	Sequence 104, App
49	14	48.3	6	4	US-09-812-283-14	Sequence 14, Appl
50	14	48.3	7	3	US-08-974-549A-375	Sequence 375, App
51	14	48.3	7	3	US-09-460-384-3	Sequence 3, Appli
52	14	48.3	7	4	US-08-912-951-142	Sequence 142, App
53	14	48.3	7	4	US-08-753-750B-18	Sequence 18, Appl
54	14	48.3	7	4	US-09-402-181B-375	Sequence 375, App
55	14	48.3	7	4	US-09-721-456-375	Sequence 375, App
56	14	48.3	7	4	US-09-672-494-11	Sequence 11, Appl
57	14	48.3	7	4	US-09-285-912A-7	Sequence 7, Appli
58	13	44.8	4	1	US-07-972-007-36	Sequence 36, Appl
59	13	44.8	4	1	US-08-351-058A-4	Sequence 4, Appli
60	13	44.8	4	1	US-08-547-618-36	Sequence 36, Appl
61	13	44.8	4	2	US-08-637-759B-131	Sequence 131, App
62	13	44.8	4	2	US-08-685-589A-31	Sequence 31, Appl
63	13	44.8	4	3	US-08-871-355A-131	Sequence 131, App
64	13	44.8	4	3	US-09-222-373-50	Sequence 50, Appl
65	13	44.8	4	3	US-09-330-970-7	Sequence 7, Appli
66	13	44.8	4	3	US-09-201-945-131	Sequence 131, App
67	13	44.8	4	3	US-09-248-074-59	Sequence 59, Appl
68	13	44.8	4	3	US-09-187-859-432	Sequence 432, App
69	13	44.8	4	4	US-09-357-717-39	Sequence 39, Appl
70	13	44.8	4	4	US-09-305-927-20	Sequence 20, Appl
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72	13	44.8	4	4	US-09-057-162-36	Sequence 36, Appl
73	13	44.8	4	4	US-09-248-015-67	Sequence 67, Appl
74	13	44.8	4	4	US-09-839-542B-432	Sequence 432, App
75	13	44.8	4	4	US-09-264-516A-20	Sequence 20, Appl
76	13	44.8	4	4	US-09-497-232-12	Sequence 12, Appl
77	13	44.8	4	4	US-09-544-782-59	Sequence 59, Appl
78	13	44.8	4	4	US-09-721-108-18	Sequence 18, Appl
79	13	44.8	4	4	US-09-721-108-116	Sequence 116, App
80	13	44.8	4	4	US-09-282-029A-3	Sequence 3, Appli
81	13	44.8	4	4	US-09-424-487B-37	Sequence 37, Appl
82	13	44.8	4	4	US-09-424-487B-51	Sequence 51, Appl
83	13	44.8	4	4	US-09-424-487B-55	Sequence 55, Appl
84	13	44.8	4	4	US-09-424-487B-56	Sequence 56, Appl
85	13	44.8	4	4	US-09-424-487B-59	Sequence 59, Appl
86	13	44.8	4	4	US-09-424-487B-61	Sequence 61, Appl
87	13	44.8	4	4	US-09-424-487B-62	Sequence 62, Appl
88	13	44.8	4	4	US-09-424-487B-102	Sequence 102, App
89	13	44.8	4	4	US-09-424-487B-103	Sequence 103, App
90	13	44.8	4	4	US-09-530-560B-22	Sequence 22, Appl
91	13	44.8	4	4	US-09-185-908-3	Sequence 3, Appli
92	13	44.8	4	4	US-09-910-706A-15	Sequence 15, Appl
93	13	44.8	4	4	US-10-058-821-39	Sequence 39, Appl
94	13	44.8	4	4	US-09-450-073-50	Sequence 50, Appl
95	13	44.8	4	4	US-09-434-355A-3	Sequence 3, Appli
96	13	44.8	4	4	FCT-US92-0996A-4	Sequence 4, Appli
97	13	44.8	5	1	US-08-351-058A-8	Sequence 8, Appli
98	13	44.8	5	1	US-08-798-897-45	Sequence 45, Appl
99	13	44.8	5	2	US-08-978-523-45	Sequence 45, Appl
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ALIGNMENTS

RESULT 1
US-09-326-718-4
; Sequence 4, Application US/09326718
; Patent No. 6303573
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: MacKenna, Deirdre A.
; TITLE OF INVENTION: Heart Homing Peptides and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-LJ 3512
; CURRENT APPLICATION NUMBER: US/09/326,718
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-326-718-4

Query Match 100.0%; Score 29; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVVTSS 7
Db 1 VLVVTSS 7
:|:|:|:|

RESULT 2
US-09-357-952-103
; Sequence 103, Application US/09357952
; Patent No. 6248904
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole-
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/09/357,952
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: US 60/093,642
; EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-357-952-103

Query Match 62.1%; Score 18; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLVVTSS 7
Db 1 VLVVTSS 7
:|:|:|:|

RESULT 3
US-09-521-650-103
; Sequence 103, Application US/09521650
; Patent No. 6395429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-521-650-103

Query Match 62.1%; Score 18; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLVVTSS 7
Db 1 VLVVTSS 7
:|:|:|:|

RESULT 4
US-09-168-888-103
; Sequence 103, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-168-888-103

Qy 1 VLVVTSS 7
Db 1 VLVVTSS 7
:|:|:|:|

US-09-168-888-103

Query Match 62.1%; Score 18; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLVVTSS 7
:||:|
Db 1 LVLASSS 7

RESULT 5

US-09-947-387-103
; Sequence 103, Application US/09947387
; Patent No. 6759207
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6759207el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-103

Query Match 62.1%; Score 18; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLVVTSS 7
:||:|
Db 1 LVLASSS 7

RESULT 6

US-08-554-591-1
; Sequence 1, Application US/08554591
; Patent No. 5834257
; GENERAL INFORMATION:
; APPLICANT: Sugano, Yasushi
; APPLICANT: Terada, Ichiro
; APPLICANT: Kodama, Hisashi
; TITLE OF INVENTION: No. 5834257el Alpha-Agarase and Production
; TITLE OF INVENTION: Process of Oligosaccharides and Monosaccharides
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch and Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/554,591
APPLICATION NUMBER: US/08/554,591
FILING DATE: 06-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1254-124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-554-591-1

Query Match 58.6%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LVTS 6
:|:|:|
Db 3 LVTS 6

RESULT 7

US-08-760-075A-33
; Sequence 33, Application US/08760075A
; Patent No. 5942429
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/760,075A
APPLICATION NUMBER: US/08/760,075A
FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19545126.0
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/309
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 33:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-760-075A-33
Query Match 55.2%; Score 16; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 LVTSS 7
Db 1 IVTSA 5
RESULT 8
US-09-338-546-33
; Sequence 33, Application US/09338546
; Patent No. 6251645
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,075
; FILING DATE: 04-DEC-1996
; APPLICATION NUMBER: DE 19545126.0
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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Best Local Similarity 60.0%; Pred. No. 4.1e+05;
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Qy 3 LVTSS 7
Db 1 IVTSA 5
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; Sequence 33, Application US/09338546
; Patent No. 6251645
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
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; FILING DATE: 04-DEC-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,075
; FILING DATE: 04-DEC-1996
; APPLICATION NUMBER: DE 19545126.0
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-338-546-33
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Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 3 LVTSS 7
Db 1 IVTSA 5
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US-08-840-204-4
; Sequence 4, Application US/08840204
; Patent No. 6103498
; GENERAL INFORMATION:
; APPLICANT: LAWRENCE, DANIEL A.
; APPLICANT: STEFANSSON, STEINGRIMUR P.
; TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR
; TYPE 1 (PAI-1) AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/840,204
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: LIVNAT, SHMUEL
;; REGISTRATION NUMBER: 33,949
;; REFERENCE/DOCKET NUMBER: 30807-20004.00
;; TELEPHONE: (202) 887-1500
;; TELEFAX: (202) 822-0168
;; TELEX: 90-4030 MRSNFOERSWSH
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-840-204-4

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Best Local Similarity 28.6%; Pred. No. 4.1e+05;
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Qy 1 VLVTS 7
Db 1 MTMTNS 7

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US-09-258-754-296
;; Sequence 296, Application US/09258754
;; Patent No. 6174687
;; GENERAL INFORMATION:
;; APPLICANT: Ruoslahti, Erkki
;; APPLICANT: Pasqualini, Renata
;; APPLICANT: Rajotte, Daniel
;; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
;; TITLE OF INVENTION: Membrane Dipeptidase
;; FILE REFERENCE: P-LJ 3443
;; CURRENT APPLICATION NUMBER: US/09/258,754
;; CURRENT FILING DATE: 1999-02-26
;; EARLIER APPLICATION NUMBER: 09/042,107
;; EARLIER FILING DATE: 1998-03-13
;; NUMBER OF SEQ ID NOS: 452
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 296
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; US-09-258-754-296

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Db 2 LVNSS 6

RESULT 12
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;; Sequence 75, Application US/08960780
;; Patent No. 6204435
;; GENERAL INFORMATION:
;; APPLICANT: Feitelson, Jerald S.
;; APPLICANT: Schnepf, H. Ernest

;; APPLICANT: Narva, Kenneth E.
;; APPLICANT: Stockhoff, Brian A.
;; APPLICANT: Schmeits, James
;; APPLICANT: Loewer, David
;; APPLICANT: Dullum, Charles Joseph
;; APPLICANT: Muller-Cohn, Judy
;; APPLICANT: Stamp, Lisa
;; TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide
;; TITLE OF INVENTION: Sequences Which Encode These Toxins
;; NUMBER OF SEQUENCES: 134
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;; STREET: 2421 N.W. 41st Street, Suite A-1
;; CITY: Gainesville
;; STATE: FL
;; COUNTRY: US
;; ZIP: 32606-6669
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/960,780
;; FILING DATE: 30-OCT-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/029,848
;; FILING DATE: 30-OCT-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Saliwanchik, David R.
;; REGISTRATION NUMBER: 31,794
;; REFERENCE/DOCKET NUMBER: MA-708
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 352-375-8100
;; TELEFAX: 352-372-5800
;; INFORMATION FOR SEQ ID NO: 75:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-960-780-75

Query Match 55.2%; Score 16; DB 3; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VLVTS 7
Db 2 LLSTSS 7

RESULT 13
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;; Sequence 296, Application US/09042107
;; Patent No. 6232287
;; GENERAL INFORMATION:
;; APPLICANT: Ruoslahti, Erkki
;; APPLICANT: Pasqualini, Renata
;; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
;; TITLE OF INVENTION: Tissues
;; FILE REFERENCE: P-LJ 2892
;; CURRENT APPLICATION NUMBER: US/09/042,107
;; CURRENT FILING DATE: 1998-03-13
;; NUMBER OF SEQ ID NOS: 436
;; SOFTWARE: PatentIn Ver. 2.0
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;; LENGTH: 7
;; TYPE: PRT
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 14

US-09-073-898-75
; Sequence 75, Application US/09073898

; Patent No. 6242669

; GENERAL INFORMATION:

; APPLICANT: Feitelson, Jerald S.

; APPLICANT: Schnepf, H. Ernest

; APPLICANT: Narva, Kenneth E.

; APPLICANT: Stockhoff, Brian A.

; APPLICANT: Schmeits, James

; APPLICANT: Loewer, David

; APPLICANT: Dullum, Charles Joseph

; APPLICANT: Muller-Cohn, Judy

; APPLICANT: Stamp, Lisa

; APPLICANT: Morrill, George

; APPLICANT: Finstad-Lee, Stacey

; TITLE OF INVENTION: No. 6242669el Pesticidal Toxins and Nucleotide

; NUMBER OF SEQUENCES: 144

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: US

; ZIP: 32606-6669

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/073,898

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/029,848

; FILING DATE: 30-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/960,780

; FILING DATE: 30-OCT-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Sanders, Jay M.

; REGISTRATION NUMBER: 39,355

; REFERENCE/DOCKET NUMBER: MA-708C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 352-375-8100

; TELEFAX: 352-372-5800

; INFORMATION FOR SEQ ID NO: 75:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-073-898-75

Query Match 55.2%; Score 16; DB 3; Length 7;

Best Local Similarity 66.7%; Pred. No. 4.1e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 410
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-410

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Best Local Similarity 100.0%; Pred.No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2005, 11:57:01 ; Search time 89.3333 Seconds
(without alignments)
30.529 Million cell updates/sec

Title: US-09-910-582B-4

Perfect score: 29

Sequence: 1 VLVVTS 7

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Searched: 1745140 seqs, 38960808 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	19	65.5	7	14	US-10-006-760-35
5	18	62.1	7	9	US-09-947-387-103
6	18	62.1	7	15	US-10-138-375-103
7	18	62.1	7	16	US-10-829-381-103
8	17	58.6	5	9	US-09-873-676-111
9	17	58.6	6	15	US-10-363-208-259
10	17	58.6	6	16	US-10-363-204-74
11	17	58.6	7	14	US-10-022-066-209
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					Sequence 4, Appli
					Sequence 35, Appl
					Sequence 103, App
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					Sequence 111, App
					Sequence 259, App
					Sequence 74, Appl
					Sequence 209, App

12	55.2	7	9	US-09-850-351A-75	Sequence 75, Appl
13	55.2	7	10	US-09-983-802-410	Sequence 410, App
14	55.2	7	10	US-09-866-050A-398	Sequence 398, App
15	55.2	7	10	US-09-984-490-410	Sequence 410, App
16	55.2	7	11	US-09-973-278-637	Sequence 637, App
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20	55.2	7	16	US-10-688-276-14	Sequence 14, Appl
21	55.2	7	17	US-10-808-187-2335	Sequence 2335, Ap
22	55.2	7	17	US-10-838-289-96	Sequence 96, Appl
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25	51.7	5	17	US-10-808-187-718	Sequence 718, App
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27	51.7	6	16	US-10-399-162-15	Sequence 15, Appl
28	51.7	6	16	US-10-343-389A-4	Sequence 4, Appli
29	51.7	6	16	US-10-641-633-87	Sequence 87, Appl
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32	51.7	7	9	US-09-950-313-46	Sequence 46, Appl
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35	51.7	7	17	US-10-808-187-83	Sequence 83, Appl
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47	48.3	6	9	US-09-071-838-14	Sequence 14, Appl
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49	48.3	6	9	US-09-727-963A-82	Sequence 82, Appl
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53	48.3	6	14	US-10-319-402-28	Sequence 28, Appl
54	48.3	6	15	US-10-138-375-104	Sequence 104, App
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58	48.3	6	16	US-10-829-381-104	Sequence 104, App
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65	48.3	6	17	US-10-666-095-15	Sequence 15, Appl
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76	48.3	7	14	US-10-325-810-375	Sequence 7, Appli
77	48.3	7	15	US-10-325-810-375	Sequence 375, App
78	48.3	7	15	US-10-243-613-7	Sequence 7, Appli
79	48.3	7	16	US-10-727-335-36	Sequence 36, Appl
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83	48.3	7	17	US-10-901-243-15	Sequence 15, Appl
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85 14 48.3 7 17 US-10-912-512-429 Sequence 429, App
86 14 48.3 7 17 US-10-235-043-243 Sequence 243, App
87 14 48.3 7 17 US-10-235-043-429 Sequence 429, App
88 14 48.3 7 17 US-10-496-507-3 Sequence 3, Appl
89 13 44.8 4 9 US-09-769-145-59 Sequence 59, Appl
90 13 44.8 4 9 US-09-264-516A-20 Sequence 20, Appl
91 13 44.8 4 9 US-09-185-908-3 Sequence 3, Appl
92 13 44.8 4 10 US-09-910-708A-15 Sequence 15, Appl
93 13 44.8 4 14 US-10-105-008-59 Sequence 59, Appl
94 13 44.8 4 14 US-10-006-869-432 Sequence 432, App
95 13 44.8 4 14 US-10-058-821-39 Sequence 39, Appl
96 13 44.8 4 14 US-10-141-357-20 Sequence 20, Appl
97 13 44.8 4 14 US-10-222-455-36 Sequence 36, Appl
98 13 44.8 4 15 US-10-359-546-67 Sequence 67, Appl
99 13 44.8 4 15 US-10-395-032-432 Sequence 432, App
100 13 44.8 4 15 US-10-425-557-59 Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-782-650-3
; Sequence 3, Application US/09782650
; Patent No. US20020019350A1
; GENERAL INFORMATION:
; APPLICANT: Levine, Arnold J.
; APPLICANT: Mitterer, Artur
; APPLICANT: Falkner, Falko-Guenter
; APPLICANT: Scheiflinger, Friedrich
; APPLICANT: Dörner, Friedrich
; APPLICANT: Edwards LifeSciences Corporation
; TITLE OF INVENTION: Targeted Angiogenesis
; FILE REFERENCE: 20553D-000611US
; CURRENT APPLICATION NUMBER: US/09/782,650
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: US 09/324,079
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 09/327,045
; PRIOR FILING DATE: 1999-06-07
; PRIOR APPLICATION NUMBER: PCT/US00/14988
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:targeting
; OTHER INFORMATION: molecule
US-09-782-650-3

Query Match 100.0%; Score 29; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVLTSS 7
| | | | |
Db 1 VLVLTSS 7

RESULT 2
US-09-910-582B-4
; Sequence 4, Application US/09910582B
; Publication No. US20030045476A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: MacKenna, Deirdre A.
; TITLE OF INVENTION: Heart Homing Conjugates
; FILE REFERENCE: P-LJ 4857
; CURRENT APPLICATION NUMBER: US/09/910,582B
; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 09/326,718
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-910-582B-4

Query Match 100.0%; Score 29; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVLTSS 7
| | | | |
Db 1 VLVLTSS 7

RESULT 3
US-10-838-289-36
; Sequence 36, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jimming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; TITLE OF INVENTION: NANOSHELLS
; FILE REFERENCE: CMRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Heart homing peptide
US-10-838-289-36

Query Match 100.0%; Score 29; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVLTSS 7
| | | | |
Db 1 VLVLTSS 7

RESULT 4
US-10-006-760-35
; Sequence 35, Application US/10006760
; Publication No. US20030186385A1
; GENERAL INFORMATION:
; APPLICANT: Koide, Shohel
; TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND
; TITLE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF
; FILE REFERENCE: 176/60901
; CURRENT APPLICATION NUMBER: US/10/006,760
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/249,756
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 7

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AB Loop
; OTHER INFORMATION: sequence for polypeptide monobody in pYT45AB7N
; OTHER INFORMATION: library
US-10-006-760-35

Query Match      65.5%; Score 19; DB 14; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VLVTS 7
   |||
Db 2 VLITRS 7

RESULT 5
US-09-947-387-103
; Sequence 103, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecule
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-103

Query Match      62.1%; Score 18; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLVTS 7
   |||
Db 1 LVLS 7

RESULT 6
US-10-138-375-103
; Sequence 103, Application US/10138375
; Publication No. US20030208037A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
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; CURRENT APPLICATION NUMBER: US/10/138,375
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-07-21
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-07-21
; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-138-375-103

Query Match      62.1%; Score 18; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLVTS 7
   |||
Db 1 LVLS 7

RESULT 7
US-10-829-381-103
; Sequence 103, Application US/10829381
; Publication No. US20040191844A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290006
; CURRENT APPLICATION NUMBER: US/10/829,381
; CURRENT FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 09/947,387
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-829-381-103

Query Match      62.1%; Score 18; DB 16; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLVTS 7
   |||
Db 1 LVLS 7

RESULT 8
US-09-873-676-111
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; Sequence 111, Application US/09873676
; Patent No. US20020077289A1
; GENERAL INFORMATION:
; APPLICANT: Macdonald, Nicholas J.
; TITLE OF INVENTION: Sim, Kim L.
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT APPLICATION NUMBER: US/09/873,676
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/289,387
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 111
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
;
US-09-873-676-111

Query Match      58.6%; Score 17; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LVTS 6
Db 1 LVTS 4

RESULT 9
US-10-363-208-259
; Sequence 259, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 259
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(6)
; OTHER INFORMATION: synthetic construct
;
US-10-363-208-259

Query Match      58.6%; Score 17; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLVT 5
Db 2 VLVT 5

RESULT 10
US-10-363-204-74
; Sequence 74, Application US/10363204
; Publication No. US20040170955A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: US/10/363,204
; CURRENT FILING DATE: 2003-03-07
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; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(6)
; OTHER INFORMATION: synthetic construct
;
US-10-363-204-74

Query Match      58.6%; Score 17; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLVT 5
Db 2 VLVT 5

RESULT 11
US-10-022-066-209
; Sequence 209, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 209
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
;
US-10-022-066-209

Query Match      58.6%; Score 17; DB 14; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVTS 6
Db 1 LVIVTT 6

RESULT 12
US-09-850-351A-75
; Sequence 75, Application US/09850351A
; Patent No. US2002010080A1
; GENERAL INFORMATION:
; APPLICANT: Feitelson, Jerald S.
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stockhoff, Brian A.
; APPLICANT: Schmeits, James
; APPLICANT: Loewer, David
; APPLICANT: Dullum, Charles Joseph
```

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; Muller-Cohn, Judy
; Stamp, Lisa
; Morrill, George
; TITLE OF INVENTION: No. US2002010080A1e1 Pesticidal Toxins and Nucleotide
; Sequences Which Encode These Toxins
;
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/850,351A
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/073,898
; FILING DATE: 06-May-1998
; APPLICATION NUMBER: US 08/960,780
; FILING DATE: 30-OCT-1997
; APPLICATION NUMBER: US 60/029,848
; FILING DATE: 30-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-708CD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 75:
;
; US-09-850-351A-75
;
; Query Match 55.2%; Score 16; DB 9; Length 7;
; Best Local Similarity 66.7%; Pred. No. 1.6e+06;
; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 2 VLVTS 7
; Db 2 LLSST 7
;
; RESULT 13
; US-09-983-802-410
; Sequence 410, Application US/09983802
; Publication No. US20030022185A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/983,802
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

```

```

Db          |||||
            4 VLVV 7

RESULT 14
US-09-866-050A-398
; Sequence 398, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c4U
; CURRENT APPLICATION NUMBER: US/09/866,050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 398
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mouse
US-09-866-050A-398

Query Match          55.2%; Score 16; DB 10; Length 7;
Best Local Similarity 33.3%; Pred. No. 1.6e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVVTS 6
Db 1 MVIIT 6

RESULT 15
US-09-984-490-410
; Sequence 410, Application US/09984490
; Publication No. US20030064412A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/984,490
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

Query Match          55.2%; Score 16; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVV 4
Db 4 VLVV 7

Search completed: August 3, 2005, 12:14:03
Job time : 91.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 12:07:52 ; Search time 38 Seconds

(without alignments)
20.256 Million cell updates/sec

Title: US-09-910-582B-9

Perfect score: 51

Sequence: 1 CLHRGNSC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 606

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	37.3	8	2	PT0368
2	18	35.3	8	2	PH0934
3	16	31.4	6	2	SI4159
4	16	31.4	7	2	B34818
5	16	31.4	8	2	C61512
6	16	31.4	8	2	D61512
7	15	29.4	7	4	I55382
8	14	27.5	6	2	A41946
9	14	27.5	7	2	S45311
10	14	27.5	8	2	S59622
11	14	27.5	8	2	PH1618
12	14	27.5	8	2	A25836
13	14	27.5	8	2	XGHUEU
14	13	25.5	5	2	B22565
15	13	25.5	6	2	C22565
16	13	25.5	6	2	I37263
17	13	25.5	6	2	B56979
18	13	25.5	6	2	I49421
19	13	25.5	7	2	PH1408
20	13	25.5	8	2	B54823
21	13	25.5	8	2	A54823
22	13	25.5	8	2	I57018
23	13	25.5	8	2	S65381
24	13	25.5	8	2	S89155
25	12	23.5	5	2	PT0695
26	12	23.5	6	2	S78764
27	12	23.5	6	2	PT0532
28	12	23.5	6	2	A43129
29	12	23.5	7	2	PQ0663
					IG gamma chain C r
					T-cell receptor be
					parasporeal crystal
					vicilin 57K chain
					variant surface gl
					variant surface gl
					hypothetical pepti
					T-cell receptor ga
					microcin C7 - Esch
					metallothionein is
					IG H chain V-D-J r
					L-serine ammonia-1
					urine glycopeptide
					R-phycoerythrin al
					R-phycoerythrin be
					Y protein - human
					collagen alpha 1(I
					laminin B1 - weate
					IG heavy chain V r
					olfactory receptor
					olfactory receptor
					gene Cfr protein
					cytochrome-c oxida
					ferredoxin a2 - Ja
					T-cell receptor be
					ribosomal protein
					T-cell receptor be
					neuropeptide GNFR
					membrane protein -

30	12	23.5	7	2	S58797	serine/threonine-s
31	12	23.5	8	2	PA0035	protein QA300039 -
32	12	23.5	8	2	A35768	T-cell receptor al
33	12	23.5	8	2	PQ0701	unidentified 6.5/3
34	12	23.5	8	2	T48890	hypothetical prote
35	11	21.6	4	2	S47552	ubiquitin - rat
36	11	21.6	5	2	PT0325	T-cell receptor be
37	11	21.6	5	2	PT0700	T-cell receptor be
38	11	21.6	5	2	PT0608	H4 histone - Afric
39	11	21.6	6	2	I51434	acetylcholinestera
40	11	21.6	7	2	A34026	T-cell receptor be
41	11	21.6	7	2	PT0620	T-cell receptor be
42	11	21.6	7	2	PT0556	T-cell receptor be
43	11	21.6	7	2	PT0542	T-cell receptor be
44	11	21.6	7	2	PT0676	T-cell receptor be
45	11	21.6	7	2	PT0581	T-cell receptor be
46	11	21.6	7	2	PT0671	T-cell receptor be
47	11	21.6	7	4	S15597	orf 4 xara 5'-regi
48	11	21.6	8	2	PT0279	IG heavy chain CRD
49	11	21.6	8	2	PT0522	T-cell receptor be
50	11	21.6	8	2	PT0547	T-cell receptor be
51	10	19.6	3	3	GKHU	growth-modulating
52	10	19.6	5	2	B31836	20K protein - Rick
53	10	19.6	5	2	F22565	R-phycoerythrin ga
54	10	19.6	5	2	T10954	hypothetical prote
55	10	19.6	6	2	JN0861	peptidyl-dipeptida
56	10	19.6	6	2	JU0355	lipopeptide WS1279
57	10	19.6	6	2	A11490	pyruvate kinase (E
58	10	19.6	7	2	S38516	mabulin II chain
59	10	19.6	7	2	S70335	endospore protein,
60	10	19.6	7	2	A12016	formylglycinamide
61	10	19.6	7	2	I46868	alpha-myosin heavy
62	10	19.6	7	4	I56695	hypothetical L2 pr
63	10	19.6	8	2	S63493	dissimilatory sulf
64	10	19.6	8	2	PC1002	leucine-tRNA ligas
65	10	19.6	8	2	A37521	R-phycoerythrin ga
66	10	19.6	8	2	A46306	spasmogenic toxin
67	10	19.6	8	2	B27867	homeotic protein U
68	10	19.6	8	2	A61467	penalbumin - Adeli
69	9	17.6	3	3	A22565	R-phycoerythrin al
70	9	17.6	4	2	I51049	metallothionein-A
71	9	17.6	4	2	S43959	IG mu chain V regi
72	9	17.6	4	2	S55238	pallidipin - assas
73	9	17.6	5	2	A33882	cadmium-binding pe
74	9	17.6	5	2	B45525	actin I - malaria
75	9	17.6	5	2	S65726	hemoglobin, extrac
76	9	17.6	6	2	I37027	protamine P1 - gor
77	9	17.6	6	2	H48394	glycoprotein compo
78	9	17.6	6	2	I67345	MHC H2-K-k cell su
79	9	17.6	6	2	I65546	MHC H2-L antigen -
80	9	17.6	6	2	PT0652	T-cell receptor be
81	9	17.6	6	2	F41946	T-cell receptor ga
82	9	17.6	6	2	S71349	beta-crystallin B2
83	9	17.6	6	2	S29881	Na+/K+-exchanging
84	9	17.6	6	4	I79564	hypothetical TCU3
85	9	17.6	6	2	B33882	cadmium-binding he
86	9	17.6	7	2	PH1602	IG H chain V-D-J r
87	9	17.6	7	2	PT0579	T-cell receptor be
88	9	17.6	7	2	A38671	peptidylglycine mo
89	9	17.6	7	2	PH0932	T-cell receptor be
90	9	17.6	7	2	A58512	venom heptapeptide
91	9	17.6	7	2	S08606	hypothetical prote
92	9	17.6	8	2	PH1407	IG heavy chain V r
93	9	17.6	8	2	PH0803	T-cell receptor al
94	9	17.6	8	2	S19288	acylase - Kluyvera
95	9	17.6	8	2	A35180	neutral proteinase
96	8	15.7	3	3	RHSHT	thyloliberin - she
97	8	15.7	3	3	A92971	thyloliberin - eas
98	8	15.7	3	3	RHTDO	thyloliberin - Bom
99	8	15.7	3	3	RHPGT	thyloliberin - pig
100	8	15.7	3	3	A60898	bursin - chicken

ALIGNMENTS

RESULT 1

PT0368
IG gamma chain C region (gamma-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Aug-1996
C;Accession: PT0368
R;Milili, M.; Fougereau, M.; Guglielmi, P.; Schiff, C.
Mol. Immunol. 28, 753-761, 1991
A;Title: Early occurrence of immunoglobulin isotype switching in human fetal liver.
A;Reference number: PT0368; MUID:91312348; PMID:1906981
A;Accession: PT0368
A;Molecule type: mRNA
A;Residues: 1-8 <MIL>
A;Experimental source: fetal liver
C;Keywords: immunoglobulin

Query Match 37.3%; Score 19; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHRG 5
| | |
Db 1 LHQG 4

RESULT 2

PH0934
T-cell receptor beta chain V-D-J region (clone 5) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0934
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A;Reference number: PH0934; MUID:92078857; PMID:1836012
A;Accession: PH0934
A;Molecule type: mRNA
A;Residues: 1-8 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
A;Note: the authors translated the codon CAG for residue 7 as Glu
C;Keywords: T-cell receptor

Query Match 35.3%; Score 18; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CLHRGN 6
| | |
Db 1 CASSGN 6

RESULT 3

S14159
paraspinal crystal protein Cry7C - Bacillus thuringiensis (fragment)
N;Alternate names: delta-endotoxin
C;Species: Bacillus thuringiensis
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C;Accession: S14159
R;Convents, D.; Cherlet, M.; van Damme, J.; Lasters, I.; Lauwereys, M.
Eur. J. Biochem. 195, 631-635, 1991
A;Title: Two structural domains as a general fold of the toxic fragment of the Bacillus
A;Reference number: S14087; MUID:91153300; PMID:1847865
A;Accession: S14159
A;Molecule type: protein
A;Residues: 1-6 <CON>

Query Match 31.4%; Score 16; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GNS 7
| | |
Db 4 GNS 6

RESULT 4

B34818
vicillin 57K chain - pigeon pea (fragment)
C;Species: Cajanus cajan (pigeon pea)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 30-Sep-1993
C;Accession: B34818
R;Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.
Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990
A;Title: Unusual denaturation properties of vicillin from Cajanus cajan.
A;Reference number: A34818; MUID:90165956; PMID:2306256
A;Accession: B34818
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MAW>

Query Match 31.4%; Score 16; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRG 5
| | |
Db 3 CMESG 7

RESULT 5

C61512
variant surface glycoprotein MITat 1.4 - Trypanosoma brucei (fragment)
C;Species: Trypanosoma brucei
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: C61512
R;Holder, A.A.; Cross, G.A.M.
Mol. Biochem. Parasitol. 2, 135-150, 1981
A;Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-termir
A;Reference number: A61512; MUID:81172836; PMID:6163983
A;Accession: C61512
A;Molecule type: protein
A;Status: preliminary
A;Residues: 1-8 <HOL>
A;Cross-references: UNIPROT:Q7M3S3
C;Keywords: glycoprotein

Query Match 31.4%; Score 16; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 NSC 8
| | |
Db 4 NAC 6

RESULT 6

D61512
variant surface glycoprotein MITat 1.6 - Trypanosoma brucei (fragment)
C;Species: Trypanosoma brucei
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: D61512
R;Holder, A.A.; Cross, G.A.M.
Mol. Biochem. Parasitol. 2, 135-150, 1981
A;Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-termir
A;Reference number: A61512; MUID:81172836; PMID:6163983
A;Accession: D61512
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <HOL>
A;Cross-references: UNIPROT:Q7M3S2
C;Keywords: glycoprotein

Query Match 31.4%; Score 16; DB 2; Length 8;

```

A;Accession: S45311
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-7 <CON>
A;Cross-references: UNIPROT:Q47505
C;Genetics:
A;Gene: mcca
A;Genome: plasmid pMcC7
C;Keywords: antibacterial
F;1/Modified site: N-formylmethionine #status predicted
F;7/Modified site: asparagine derivative (Asn) #status experimental

Query Match 27.5%; Score 14; DB 2; Length 7;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0;

Qy 2 LHRGS 7
Db 1 MRTGNA 6

RESULT 10
S59622
metallothionein isoform a, cadmium-binding - Ariantha arbustorum (te)
C;Species: Ariantha arbustorum
C;Date: 19-Mar-1997 #sequence_revision 24-Oct-1997 #text_change 09-9
C;Accession: S59622
R;Berger, B.; Hunziker, P.E.; Hauer, C.R.; Birchler, N.; Dallinger,
Biochem. J. 311, 951-957, 1995
A;Title: Mass spectrometry and amino acid sequencing of two cadmium
A;Reference number: S59621; MUID:96067616; PMID:7487956
A;Accession: S59622
A;Molecule type: protein
A;Residues: 1-8 <BER>
A;Cross-references: UNIPROT:P55946
C;Superfamily: metallothionein
C;Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 27.5%; Score 14; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0;

Qy 6 NSC 8
Db 3 SSC 5

RESULT 11
PH1618
Ig H chain V-D-J region (clone B-less 33) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-9
C;Accession: PH1618
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1618
A;Molecule type: DNA
A;Residues: 1-8 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 27.5%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0;

Qy 1 CLHRG 5
Db 1 CARHG 5

RESULT 12

```

A25836
 L-serine ammonia-lyase (EC 4.3.1.17) - Escherichia coli (fragment)
 C;Species: Escherichia coli
 C;Date: 24-Jan-1988 #sequence_revision 24-Jan-1988 #text_change 09-Jul-2004
 R;Accession: A25836
 R;Heincz, M.C.; McFall, E.
 J. Bacteriol. 123, 1163-1168, 1975
 A;Title: N-terminal amino acid sequences of D-serine deaminases of wild-type and operat
 A;Reference number: A25836; MUID:76005414; PMID:1099073
 A;Contents: K12
 A;Accession: A25836
 A;Molecule type: protein
 A;Residues: 1-8 <HEI>
 A;Cross-references: UNIPROT:Q7M194
 C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; seri

Query Match 27.5%; Score 14; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 GNSC 8
 DB 5 GRHC 8

RESULT 13
 XGHUEU
 urine glycopeptide - human
 C;Species: Homo sapiens (man)
 C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004
 R;Accession: A03188
 R;Lote, C.J.; Weiss, J.B.
 Biochem. J. 123, 25P, 1971
 A;Title: Identification in urine of a low-molecular-weight polar glycopeptide containing
 A;Reference number: A03188; MUID:72062338; PMID:5126885
 A;Accession: A03188
 A;Molecule type: protein
 A;Residues: 1-8 <LOT>
 A;Cross-references: UNIPROT:P02729
 C;Comment: The identity of the glycoprotein from which this peptide is derived is unknown
 re has also been found (see PIR:XGHUEU).
 C;Keywords: glycoprotein
 F;1/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 27.5%; Score 14; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CLH 3
 DB 1 CEH 3

RESULT 14
 B22565
 R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)
 C;Species: Gastroclonium coulteri
 C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
 R;Accession: B22565
 R;Klotz, A.V.; Glazer, A.N.
 J. Biol. Chem. 260, 4856-4863, 1985
 A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
 A;Reference number: A22565; MUID:85182601; PMID:3886644
 A;Accession: B22565
 A;Molecule type: protein
 A;Residues: 1-5 <KLO>

Query Match 25.5%; Score 13; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CLHR 4
 DB 1

Db 2 CVPR 5
 RESULT 15
 C22565
 R-phycoerythrin beta-1 chain - red alga (Gastroclonium coulteri) (fragment)
 C;Species: Gastroclonium coulteri
 C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
 R;Accession: C22565
 R;Klotz, A.V.; Glazer, A.N.
 J. Biol. Chem. 260, 4856-4863, 1985
 A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
 A;Reference number: A22565; MUID:85182601; PMID:3886644
 A;Accession: C22565
 A;Molecule type: protein
 A;Residues: 1-6 <KLO>

Query Match 25.5%; Score 13; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CL 2
 DB 4 CL 5

Search completed: August 3, 2005, 12:20:25
 Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 12:03:27 ; Search time 171 Seconds
(without alignments)
23.957 Million cell updates/sec

Title: US-09-910-582B-9

Perfect score: 51

Sequence: 1 CLHRGNSC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	45.1	8	2	Q6XFW6 anthreptes
2	20	39.2	8	2	Q6HOC6 isoetes fla
3	17	33.3	8	2	Q37854 bacterioph
4	16	31.4	7	2	Q66113 cherry leaf
5	16	31.4	8	2	Q7M3S2 trypanosoma
6	16	31.4	8	2	Q7M3S3 trypanosoma
7	15	29.4	7	2	Q67113 influenza a
8	15	29.4	8	2	Q28866 megaptera n
9	14	27.5	7	2	Q47505 escherichia
10	14	27.5	8	1	GLUR_HUMAN
11	14	27.5	8	2	Q7M194 escherichia
12	13	25.5	5	1	TPIS CANFA
13	13	25.5	7	1	TV51 LITRU
14	13	25.5	7	2	Q42564 litorea rub
15	13	25.5	8	1	COXG_RAT
16	13	25.5	8	2	Q15890 homo sapien
17	13	25.5	8	2	Q9Y4X6 homo sapien
18	13	25.5	8	2	O02831 cryptolagus
19	13	25.5	8	2	Q7M1F1 raphanus sa
20	13	25.5	8	2	Q7M056 mus sp. gen
21	13	25.5	8	2	Q80WD5 mus spretus
22	13	25.5	8	2	Q80WD6 mus musculus
23	13	25.5	8	2	Q84156 orf virus.
24	12	23.5	6	1	FARP MONEX
25	12	23.5	6	1	TMOF_SARBU
26	12	23.5	7	2	UN06_PINPS
27	12	23.5	7	2	Q66205 transmissib
28	12	23.5	8	1	CLIP_THICU
29	12	23.5	8	2	Q15889 homo sapien
30	12	23.5	8	2	Q7Z6G0 homo sapien
31	12	23.5	8	2	Q8MUN6 heliconius

32	12	23.5	8	2	Q9GD00	Q9GD00 masoala mad
33	12	23.5	8	2	Q699J0	Q699J0 beta vulgar
34	12	23.5	8	2	Q6ZZ01	Q6ZZ01 silene con
35	12	23.5	8	2	Q6ZZ02	Q6ZZ02 lychnis cor
36	12	23.5	8	2	Q7MIU0	Q7MIU0 oryza sativ
37	12	23.5	8	2	Q9JLD7	Q9JLD7 nesocricetu
38	12	23.5	8	2	Q7ZPJ1	Q7ZPJ1 human immun
39	11	21.6	5	1	UXA4_CHLTR	P38005 chlamydia t
40	11	21.6	7	1	UF04_MOUSE	R38642 mus musculu
41	11	21.6	7	2	Q8GLI2	Q8GLI2 borrelia bu
42	11	21.6	7	2	Q63480	Q63480 rattus norv
43	11	21.6	8	1	ALL5_CYDPO	P82156 cydia pomon
44	11	21.6	8	2	Q15888	Q15888 homo sapien
45	11	21.6	8	2	Q69YH8	Q69YH8 homo sapien
46	11	21.6	8	2	Q9UHK1	Q9UHK1 homo sapien
47	11	21.6	8	2	Q7RBP6	Q7RBP6 plasmodium
48	11	21.6	8	2	Q9AVA0	Q9AVA0 varanus sem
49	11	21.6	8	2	Q6YLT8	Q6YLT8 sciadopitys
50	11	21.6	8	2	Q70Y68	Q70Y68 prostanther
51	11	21.6	8	2	Q70Y69	Q70Y69 syncolostem
52	11	21.6	8	2	Q70Y84	Q70Y84 plectranthu
53	11	21.6	8	2	Q32560	Q32560 escherichia
54	11	21.6	8	2	P83531	P83531 lactobacill
55	11	21.6	8	2	Q56429	Q56429 thermus the
56	11	21.6	8	2	Q79AG6	Q79AG6 pantoea agg
57	11	21.6	8	2	Q7T863	Q7T863 largemouth
58	10	19.6	3	1	GRWM_HUMAN	P01157 homo sapien
59	10	19.6	5	1	AP21_EISFO	P84182 eisenia foe
60	10	19.6	7	2	Q28742	Q28742 oryctolagus
61	10	19.6	7	2	Q9CSB3	Q9CSB3 arabidopsis
62	10	19.6	7	2	P72081	P72081 nocardia la
63	10	19.6	8	1	ANG2_BOTJA	Q10582 bothrops ja
64	10	19.6	8	1	COM2_CONPU	P58785 conus purpu
65	10	19.6	8	1	LCK1_LEUMA	P21140 leucophaea
66	10	19.6	8	1	LCK3_LEUMA	P21142 leucophaea
67	10	19.6	8	1	PK1_PERAM	P82685 periplaneta
68	10	19.6	8	1	PK3_PERAM	P82689 periplaneta
69	10	19.6	8	1	PK5_PERAM	P82691 phoneutria
70	10	19.6	8	1	TXVI_PHONI	Q7M3P1 phoneutria
71	10	19.6	8	2	Q05403	Q05403 saccharomyc
72	10	19.6	8	2	Q16468	Q16468 homo sapien
73	10	19.6	8	2	Q81V87	Q81V87 homo sapien
74	10	19.6	8	2	Q6LD47	Q6LD47 homo sapien
75	10	19.6	8	2	Q7Z4N9	Q7Z4N9 homo sapien
76	10	19.6	8	2	Q9BYV5	Q9BYV5 homo sapien
77	10	19.6	8	2	Q7RC74	Q7RC74 plasmodium
78	10	19.6	8	2	Q9BF82	Q9BF82 ursus arcto
79	10	19.6	8	2	Q9BF83	Q9BF83 canis fami
80	10	19.6	8	2	Q9BF84	Q9BF84 panthera on
81	10	19.6	8	2	Q9BF85	Q9BF85 leopardus p
82	10	19.6	8	2	Q9BF86	Q9BF86 felis silve
83	10	19.6	8	2	Q9BF87	Q9BF87 tapirus ind
84	10	19.6	8	2	Q9BF88	Q9BF88 equus cabal
85	10	19.6	8	2	Q9BF89	Q9BF89 okapia john
86	10	19.6	8	2	Q9BF90	Q9BF90 tragelaphus
87	10	19.6	8	2	Q9BF91	Q9BF91 hippopotamu
88	10	19.6	8	2	Q9BF94	Q9BF94 nycteris th
89	10	19.6	8	2	Q9BF95	Q9BF95 roussettus l
90	10	19.6	8	2	Q9BF96	Q9BF96 pteropus gi
91	10	19.6	8	2	Q9BF97	Q9BF97 artibeus ja
92	10	19.6	8	2	Q9BF98	Q9BF98 callimico g
93	10	19.6	8	2	Q9BF99	Q9BF99 hylobates c
94	10	19.6	8	2	Q9BFA0	Q9BFA0 macaca mula
95	10	19.6	8	2	Q9BFA1	Q9BFA1 ateles fusc
96	10	19.6	8	2	Q9BFA2	Q9BFA2 tarsius ban
97	10	19.6	8	2	Q9BFA3	Q9BFA3 lemur catta
98	10	19.6	8	2	Q9BFA4	Q9BFA4 tupiaa mino
99	10	19.6	8	2	Q9BFA5	Q9BFA5 cynocephalu
100	10	19.6	8	2	Q9BFA6	Q9BFA6 crycteropus

ALIGNMENTS

RESULT 1

Q6XFW6 PRELIMINARY; PRT; 8 AA.
 AC Q6XFW6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cytochrome oxidase III (Fragment).
 GN Name=COX3;
 OS Anthreptes collaris (collared sunbird).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;
 OC Nectariniidae; Anthreptes.
 OC NCBI_TaxID=208075;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Bowie R.C.K., Hackett S.J., Fjeldsaa J., Crowe T.M.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY234003; AAF69784.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 884 MW; F7A5B1EDC6D1EDD6 CRC64;

Query Match 45.1%; Score 23; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRGNSC 8

Db 3 HQHSC 8

RESULT 2

Q6HOC6 PRELIMINARY; PRT; 8 AA.
 AC Q6HOC6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Leafy (Fragment).
 OS Isoetes flaccida.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Lycopodiophyta; Isoetopsida; Isoetales; Isoetaceae; Isoetes.
 OC NCBI_TaxID=49763;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Hoot S.B., Napier N.S., Taylor W.Carl.;
 RT "Revealing unknown or extinct lineages within Isoetes (Isoetaceae)
 using DNA sequences from hybrids.";
 RL Am. J. Bot. 91:899-904 (2004).
 DR EMBL; AY541784; AAS79402.1; -.
 FT NON TER 1 1
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 918 MW; 3921B76EB33B1864 CRC64;

Query Match 39.2%; Score 20; DB 2; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.6e+06;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 RGNSC 8

Db 1 RGEKC 5

RESULT 3

Q37854 PRELIMINARY; PRT; 8 AA.
 AC Q37854;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Coliphage gene of unknown function, 5'end. (Fragment).
 OS Bacteriophage R17.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Levivirus.
 OC NCBI_TaxID=12026;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=73224987; PubMed=4352721;
 RA Rensing U.F.E.;
 RT "A sequence of seventy-three nucleotides from the coliphage R17
 genome.";
 RL Biochem. J. 131:593-604 (1973).
 DR EMBL; M24820; AAA72755.1; -.
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 969 MW; ECB45412C1E72726 CRC64;

Query Match 33.3%; Score 17; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 LHRGNS 7

Db 3 LHVRNS 8

RESULT 4

Q66113 PRELIMINARY; PRT; 7 AA.
 AC Q66113;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE C-terminus of the viral replicase (Fragment).
 OS Cherry leaf roll virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
 OC Nepovirus; Subgroup C.
 OC NCBI_TaxID=12615;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Walnut;
 RX MEDLINE=96124520; PubMed=8560786;
 RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
 RT "Long, nearly identical untranslated sequences at the 3' terminal
 regions of the genomic RNAs of cherry leafroll virus (walnut
 strain).";
 RL Virus Genes 10:245-252 (1995).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Walnut;
 RA Borja M.;
 RL Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA.
 DR EMBL; Z34265; CAA84019.1; -.
 FT NON TER 1 1
 FT NON TER 7 7
 SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 31.4%; Score 16; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 1.6e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CLHR 4

Db 4 CLPR 7

RESULT 5

Q7M3S2 PRELIMINARY; PRT; 8 AA.
 AC Q7M3S2;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Variant surface glycoprotein Mitat 1.6 (Fragment).

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OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE
RX MEDLINE=81172836; PubMed=6163983; DOI=10.1016/0166-6851(81)90095-5;
RA Holder A.A., Cross G.A.M.;
RT "Glycopeptides from variant surface glycoproteins of Trypanosoma
RT brucei. C-terminal location of antigenically cross-reacting
RT carbohydrate moieties.";
RL Mol. Biochem. Parasitol. 2:135-150(1981).
DR PIR; D61512; D61512. 1
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 967 MW; 74033EALAB187B03 CRC64;

Query Match 31.4%; Score 16; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GNSC 8
DB 3 GATC 6

RESULT 6
Q7M3S3
ID Q7M3S3 PRELIMINARY; PRT; 8 AA.
AC Q7M3S3; 2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Variant surface glycoprotein MITat 1.4 (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE.
RX MEDLINE=81172836; PubMed=6163983; DOI=10.1016/0166-6851(81)90095-5;
RA Holder A.A., Cross G.A.M.;
RT "Glycopeptides from variant surface glycoproteins of Trypanosoma
RT brucei. C-terminal location of antigenically cross-reacting
RT carbohydrate moieties.";
RL Mol. Biochem. Parasitol. 2:135-150(1981).
DR PIR; C61512; C61512. 1
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 979 MW; 74033EBDD444B03 CRC64;

Query Match 31.4%; Score 16; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 NSC 8
DB 4 NAC 6

RESULT 7
Q67113
ID Q67113 PRELIMINARY; PRT; 7 AA.
AC Q67113;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Influenza virus type A (Udorn/72) hemagglutinin (seg 4) cDNA, 3' end.
DE (Fragment).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=81001892; PubMed=7407922; DOI=10.1016/0092-8674(80)90486-9;
RA Dhar R., Chanock R.M., Lai C.-J.;
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza
RT viral mRNA deduced from cloned complete genomic sequences.";
RL Cell 21:495-500(1980).
DR EMBL; M25045; AAA43202.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 29.4%; Score 15; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 RGNSC 8
DB 2 RCNIC 6

RESULT 8
Q28866
ID Q28866 PRELIMINARY; PRT; 8 AA.
AC Q28866;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Actin protein (Fragment).
GN Name=actin;
OS Megaptera novaeangliae (Humpback whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaenopteridae; Megaptera.
OX NCBI_TaxID=9773;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94285813; PubMed=7912407;
RA Palumbi S.R., Baker C.S.;
RT "Contrasting population structure from nuclear intron sequences and
RT mtDNA of humpback whales.";
RL Mol. Biol. Evol. 11:426-435(1994).
DR EMBL; S73467; AAD14118.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 906 MW; 69C866D1F177408 CRC64;

Query Match 29.4%; Score 15; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRG 5
DB 5 HQG 7

RESULT 9
Q47505
ID Q47505 PRELIMINARY; PRT; 7 AA.
AC Q47505;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MccA protein.
DE Name=mccA;
OS Escherichia coli.
OG Plasmid pMccC7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9609297; PubMed=8522520;
RA Gonzalez-Pastor J.E., San Millan J.L., Castilla M.A., Moreno F.;
RT "Structure and organization of plasmid genes required to produce the
RT translation inhibitor microcin C7.";
RL J. Bacteriol. 177:7131-7140(1995).

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RN [2]
RP SEQUENCE FROM N.A.
RA San Millan J.L.;
RL Submitted (FEB-1991) to the EMBL/GenBank/DBJ databases.
DR EMBL; X57583; CAA40808.1; -.
DR PIR; S45311; S45311.
KW plasmid.
SQ SEQUENCE 7 AA; 763 MW; 644DD44861B406F0 CRC64;

Query Match 27.5%; Score 14; DB 2; Length 7;
Best Local Similarity 33.3%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LHEGNS 7
DB 1 MRTGNA 6

RESULT 10
ID GLUR_HUMAN STANDARD; PRT; 8 AA.
AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) (Fragment).
GN Urine glycopeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72062338; PubMed=5126885;
RA Lote C.J., Weiss J.B.;
RT "Identification in urine of a low-molecular-weight highly polar glycopeptide containing cysteinyl-galactose.";
RL Biochem J. 123:25P-25P(1971).
CC -1- FUNCTION: The identity of the glycoprotein from which this peptide is derived is unknown. No physiological function has been attributed. An erythrocyte membrane glycopeptide having a similar structure has also been found.
CC CC
CC PIR; A03188; XGHUEU.
DR GO; GO:0005576; C:extracellular; NAS.
KW Direct protein sequencing; Glycoprotein.
FT CARBOHYD 1 S-linked (Gal. .).
SQ SEQUENCE 8 AA; 855 MW; C2D87AA1P5B1EB1E CRC64;

Query Match 27.5%; Score 14; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CLH 3
DB 1 CEH 3

RESULT 11
ID Q7M194 PRELIMINARY; PRT; 8 AA.
AC Q7M194;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE L-serine ammonia-lyase (EC 4.3.1.17) (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE.
RX MEDLINE=76005414; PubMed=1099073;
RA Heinicz M.C., McFall E.;
RT "N-terminal amino acid sequences of D-serine deaminases of wild-type

RT and operator-constitutive strains of Escherichia coli K-12.";
RL J. Bacteriol. 123:1163-1168(1975).
DR PIR; A25836; A25836.
DR GO; GO:0003941; F:L-serine ammonia-lyase activity; IEA.
FT NON_TER 8
SQ SEQUENCE 8 AA; 906 MW; F7B1F40865BB05B6 CRC64;

Query Match 27.5%; Score 14; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GNSC 8
DB 5 GRHC 8

RESULT 12
ID TPIS_CANFA STANDARD; PRT; 5 AA.
AC P54714;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) (Fragment).
GN Name-TPil;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone phosphate.
CC -1- PATHWAY: Plays an important role in several metabolic pathways.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: Belongs to the triosephosphate isomerase family.
DR HSC-2DPAGE; P54714; DOG.
DR InterPro; IPR000652; Triophos_ismrse.
DR PROSITE; PS00171; TIM; PARTIAL.
KW Direct protein sequencing; Fatty acid biosynthesis; Gluconeogenesis; Glycolysis; Isomerase; Pentose shunt.
FT NON_TER 1 1
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;

Query Match 25.5%; Score 13; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 GNS 7
DB 3 GNN 5

RESULT 13
ID TV51_LITRU STANDARD; PRT; 7 AA.
AC P82065;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tryptophyllin S.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Pelodyadinae; Litoria.

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OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: May act as a neuromodulator or neurotransmitter.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -1- MASS SPECTROMETRY: MW=965; METHOD=FAB; RANGE=1-7; NOTE=Ref.1.
 KW Amidation; Amphibian defense peptide; Direct protein sequencing;
 KW Neuropeptide; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD_RES 7 7 Arginine amide.
 SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

 Query Match 25.5%; Score 13; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 HR 4
 DB 6 HR 7

 RESULT 14
 ID 042564 PRELIMINARY; PRT; 7 AA.
 AC 042564;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
 GN Name=Scn8a;
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontoidea; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97442476; PubMed=9295353; DOI=10.1074/jbc.272.38.24008;
 RA Plummer N.W., McBurney M.W., Meisler M.H.;
 RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
 RT two-domain protein in fetal brain and non-neuronal cells.";
 RL J. Biol. Chem. 272:24008-24015(1997).
 DR EMBL; U97673; AAB80916.1; -;
 DR GO; GO:0005216; F:ion channel activity; IEA.
 KW Ionic channel.
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

 Query Match 25.5%; Score 13; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 CL 2
 DB 5 CL 6,

 RESULT 15
 COXS_RAT
 ID _COXS_RAT STANDARD; PRT; 8 AA.
 AC P80430;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Cytochrome c oxidase polypeptide V1b (EC 1.9.3.1) (Cytochrome c
 DE oxidase subunit AED) (Fragment).
 GN Name=Cox6b1; Synonyms=Cox6b;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=95324529; PubMed=7601105;
 RA Schaegger H., Noack H., Halangk W., Brandt U., von Jagow G.;
 RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
 RT amino-terminal sequences suggest identity of the fetal heart and the
 RT adult liver isoform.";
 RL Eur. J. Biochem. 230:235-241(1995).
 CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide
 CC chains of cytochrome c oxidase, the terminal oxidase in
 CC mitochondrial electron transport. This protein may be one of the
 CC heme-binding subunits of the oxidase.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase V1b family.
 DR PIR; S65381; S65381.
 KW Direct protein sequencing; Mitochondrion; Oxidoreductase.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 1039 MW; 8101E9CAA73AE456 CRC64;

 Query Match 25.5%; Score 13; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 HR 4
 DB 7 HR 8

 Search completed: August 3, 2005, 12:19:42
 Job time : 173 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:58:21 ; Search time 159 Seconds
(without alignments)
19.460 Million cell updates/sec

Title: US-09-910-582B-9
Perfect score: 51
Sequence: 1 CLHRGNSC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 160390

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseq1980s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001s:.*
5: Geneseq2002s:.*
6: Geneseq2003as:.*
7: Geneseq2003bs:.*
8: Geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	8	4	AAB30898 Peptide w
2	51	100.0	8	4	AAB59303 Heart hom
3	31	60.8	8	3	AAV63252 Protocadh
4	30	58.8	8	2	AAV48836 Membrane
5	30	58.8	8	3	AAV61138 Cadherin-
6	30	58.8	8	5	ABG35010 Endostati
7	30	58.8	8	5	ABJ04479 HUVEC cel
8	29	56.9	8	2	AAV48662 Membrane
9	28	54.9	8	2	AAV48879 Membrane
10	28	54.9	8	5	ABB98083 FC effect
11	28	54.9	8	5	ABB98084 FC effect
12	27	52.9	8	5	ABJ04391 HUVEC cel
13	27	52.9	8	5	ABB98080 FC effect
14	26	51.0	7	2	AAV54868 Homo sapi
15	26	51.0	8	2	AAV96348 RGD cycli
16	26	51.0	8	2	AAV13414 Brain hom
17	26	51.0	8	3	AAB17981 MMP inhib
18	26	51.0	8	3	AAV63634 Desmoglei
19	26	51.0	8	3	AAB07390 Brain hom
20	26	51.0	8	4	AAE11796 Phage pep
21	26	51.0	8	5	ABG35024 Endostati
22	26	51.0	8	5	ABG34980 Human pro
23	26	51.0	8	5	ABB45686 Desmoglei
24	26	51.0	8	5	AAU10707 Brain hom
25	26	51.0	8	5	ABB73318 Exemplary

99 23 45.1 8 2 AAY48639 Aay48639 Membrane
100 23 45.1 8 3 AAY63935 Aay63935 Desmocoll

ALIGNMENTS

RESULT 1

AAB30898
ID AAB30898 standard; peptide; 8 AA.

XX AC AAB30898;
XX DT 02-APR-2001 (first entry)
XX DE Peptide which selectively binds to normal cardiac endothelium.
XX DE Cardiac endothelium; angiogenic factor; vascular endothelium;
XX KW peripheral vascular disease; cardiovascular disease; angiogenesis;
XX KW cardiac neovascularisation.
XX XX

OS Unidentified.

XX WO2000075329-A1.

XX 14-DEC-2000.

XX 31-MAY-2000; 2000WO-US014988.

XX 07-JUN-1999; 99US-00327045.

XX (EDWA-) EDWARDS LIFESCIENCES CORP.
XX (BAXT) BAXTER AG.

XX Levine AJ, Mitterer A, Falkner F, Scheifflinger F, Dörner F;
XX WPI; 2001-091212/10.

XX New chimeric molecules having an angiogenic factor linked to a targeting
PT molecule that binds to a vascular endothelium, useful for increasing
PT cardiac neovascularization, or treating peripheral vascular and
PT cardiovascular diseases.

XX Disclosure; Page 27; 67pp; English.

XX AAB30895-99 represent targeting molecules, which are used to produce the
CC chimeric molecules of the invention. AAB30895-98 selectively bind to
CC normal cardiac endothelium. The specification describes a chimeric
CC molecule comprising an angiogenic factor linked to a targeting molecule
CC that specifically binds to a vascular endothelium. The chimeric molecules
CC are useful for treatment of peripheral vascular or cardiovascular
CC diseases. Specifically, they are useful for inducing or inhibiting
CC angiogenesis, for increasing cardiac neovascularisation in ischemic
CC tissue in the peripheral vascular system

XX Sequence 8 AA;

Query Match 100.0%; Score 51; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
Db 1 CLHRGNSC 8
|||||||

RESULT 2

AAB59303
ID AAB59303 standard; peptide; 8 AA.

XX AAB59303;

XX 21-MAR-2001 (first entry)

XX Heart homing peptide SEQ ID NO: 9.
DE
XX Heart homing peptide; cardiovascular disease; ischaemic disease;
KW gene therapy.
XX Synthetic.

XX Key Location/Qualifiers

XX Disulfide-bond 1..8 /note= "disulfide bond cyclises the peptide"

XX WO2000075174-A1.

XX 14-DEC-2000.

XX 31-MAY-2000; 2000WO-US015088.

XX 07-JUN-1999; 99US-00326718.

XX (BURN-) BURNHAM INST.

XX Ruoslahti E, Mackenna DA;

XX WPI; 2001-071059/08.

XX Novel heart homing peptide that selectively homes to normal ischemic and
PT cardiac tissue useful for targeting ischemic tissues for treating
PT ischemic and cardiovascular diseases such as atherosclerosis and
PT restenosis.

XX Claim 2; Page 55; 70pp; English.

XX The present invention provides a number of heart homing peptides which
CC selectively home to cardiac tissue. These can be used in the treatment of
CC cardiovascular and ischaemic diseases, such as atherosclerosis, myocardial
CC thrombosis, restenosis, vasculitis, atherosclerotic aneurysms, myocardial
CC hypertrophy, congenital heart diseases, ischaemic heart disease and
CC anginas, acquired valvular/endocardial diseases, primary myocardial
CC diseases, cardiac tumours and arrhythmias

XX Sequence 8 AA;

Query Match 100.0%; Score 51; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
Db 1 CLHRGNSC 8
|||||||

RESULT 3

AAY63252
ID AAY63252 standard; peptide; 8 AA.

XX AAY63252;

XX 02-MAR-2000 (first entry)

DE Protocadherin cell adhesion recognition cyclic peptide SEQ ID NO:2736.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.

XX Synthetic.

OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT Disulfide-bond 1. .8
XX PN WO9957149-A2.
XX PD 11-NOV-1999.
XX PF 05-MAY-1999; 99WO-CA000363.
XX PR 05-MAY-1998; 98US-00073040.
XX PR 06-NOV-1998; 98US-00187859.
XX PR 20-JAN-1999; 99US-00234395.
XX PR 08-MAR-1999; 99US-00264516.
XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX PI Blaschuk OW, Gour BJ, Byers S;
XX DR WPI; 2000-038791/03.
XX PT New cadherin modulating agents, used for modulating nonclassical cadherin
XX PT-mediated functions for treating e.g. cancers, obesity, rheumatoid
XX PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX PS Claim 84; Page 201; 252pp; English.
XX CC The present invention describes cadherin modulating agents (MA)
XX CC comprising peptides which comprise a nonclassical cadherin cell adhesion
XX CC recognition (CAR) sequence. The MA can be used for modulating
XX CC nonclassical cadherin-mediated functions. They can be used for e.g.
XX CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
XX CC mammal, enhancing delivery of a drug through the skin of a mammal,
XX CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
XX CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
XX CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
XX CC expressing cell, preventing or treating obesity in a mammal, stimulating
XX CC blood vessel regression in a mammal, enhancing drug delivery to the
XX CC central nervous system, treating a demyelinating neurological disease,
XX CC increasing vasopermeability in a mammal, enhancing adhesion of
XX CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
XX CC a mammal, or preventing pregnancy in a mammal. They can also be used for
XX CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
XX CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
XX CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
XX CC -related macular degeneration, multiple sclerosis and diabetes. The
XX CC products can also be used for detection and diagnosis and in bioreactors.
XX CC AAY60592 to AAY64572 represent specifically claimed peptides, and
XX CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
XX CC the exemplification of the present invention
XX SQ Sequence 8 AA;

Query Match 60.8%; Score 31; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
|:|:|
Db 1 CINRDNGC 8

RESULT 4
AAY48836
ID AAY48836 standard; peptide; 8 AA.
XX AC AAY48836;
XX AC
XX AC
DT 20-MAR-2003 (revised)
DT 10-DEC-1999 (first entry)
XX DE Membrane dipeptidase-binding retina homing peptide #22.
XX

KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
KW membrane dipeptidase.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9946284-A2.
XX PD 16-SEP-1999.
XX PF 10-MAR-1999; 99WO-US005284.
XX PR 13-MAR-1998; 98US-00042107.
XX PR 26-FEB-1999; 99US-00258754.
XX PA (BURN-) BURNHAM INST.
XX PI Rajotte D, Pasqualini R, Ruoslahti EI;
XX DR WPI; 1999-571717/48.
XX PT New peptides which selectively home to organs or tissues, used for, e.g.
XX PT identifying target ligands and for therapy of pathological conditions.
XX PS Claim 28; Page 149; 193pp; English.
XX CC The present invention describes peptides that selectively home to a
XX CC tissue or organ. The peptides can be used for identifying an organ or
XX CC tissue, for identifying a target molecule expressed by an organ or tissue
XX CC or for treating an organ or tissue pathology, where the organ or tissue
XX CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,
XX CC adrenal gland, liver, and lymph node. The peptide bind to the membrane
XX CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are
XX CC used in the exemplification of the present invention. (Updated on 20-MAR-
XX CC 2003 to correct PR field.)
XX SQ Sequence 8 AA;

Query Match 58.8%; Score 30; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
|:|:|
Db 1 CMSIGNNC 8

RESULT 5
AAY61138
ID AAY61138 standard; peptide; 8 AA.
XX AC AAY61138;
XX AC
XX AC
DT 02-MAR-2000 (first entry)
XX DE Cadherin-6 cell adhesion recognition cyclic peptide SEQ ID NO:1084.
XX KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
XX KW inhibition; cadherin extracellular domain; cell adhesion recognition;
XX KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
XX KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
XX KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
XX KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
XX KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
XX KW neurological disease; cyclic.
XX OS Synthetic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Disulfide-bond 1. .8
XX

PN WO9957149-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1999; 99WO-CA000363.
 XX
 PR 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 XX 08-MAR-1999; 99US-00264516.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Gour BJ, Byers S;
 XX
 DR WPI; 2000-038791/03.
 XX
 XX New cadherin modulating agents, used for modulating nonclassical cadherin
 PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 PS Claim 27; Page 167; 252pp; English.
 XX
 CC The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MA can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC -related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 8 AA;
 Query Match 58.8%; Score 30; DB 3; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CLHRGNSC 8
 | : |||
 Db 1 CIDSGNCC 8
 RESULT 6
 ID ABG35010
 XX ABG35010 standard; peptide; 8 AA.
 AC ABG35010;
 XX
 XX 15-JUL-2002 (first entry)
 DT Endostatin targeting peptide #9.
 DE
 DE
 XX Targeting peptide; cancer; Hodgkin's disease; cytostatic;
 KW immunosuppressive; anti-inflammatory; antiarthritic; antiviral;
 KW antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;
 KW inflammatory disease; arthritis; atherosclerosis; cancer;
 KW autoimmune disease; bacterial infection; viral infection.

XX OS Unidentified.
 XX WO200220722-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 07-SEP-2001; 2001WO-US027702.
 XX
 PR 08-SEP-2000; 2000US-0231366P.
 PR 17-JAN-2001; 2001US-00765101.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Arap W, Pasqualini R;
 XX
 DR WPI; 2002-383050/41.
 XX
 XX Identifying targeting peptides useful for treating e.g. diabetes
 PT mellitus, inflammatory diseases, cancer, or autoimmune diseases,
 PT comprises exposing a sample to a phage display library and recovering
 PT phage bound to the sample.
 XX
 PS Claim 56; Page 238; 298pp; English.
 XX
 CC This invention relates to a novel method for identifying disease
 CC targeting peptides. The method comprises exposing a sample from an organ,
 CC tissue or cell type of interest, to a phage display library and
 CC recovering phage bound to the sample (the phage expresses targeting
 CC peptides). The peptides identified by the method of the invention may
 CC have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,
 CC antiatherosclerotic, antidiabetic, antibacterial and antiviral
 CC activities. The methods and composition are useful for identifying
 CC targeting peptides and one or more receptors for a targeting peptide. The
 CC targeting peptides are used for selective delivery of therapeutic agents,
 CC including gene therapy vectors and fusion proteins, to specific organs,
 CC tissues, or cell types in subject. The targeting peptide may also be used
 CC for treating diseases such as diabetes mellitus, inflammatory diseases,
 CC arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and
 CC viral infections and Hodgkin's disease. The present sequence represents a
 CC targeting peptide of the invention
 XX
 SQ Sequence 8 AA;
 Query Match 58.8%; Score 30; DB 5; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CLHRGNSC 8
 | : |||
 Db 1 CWRGSGTC 8
 RESULT 7
 ID ABJ04479
 XX ABJ04479 standard; peptide; 8 AA.
 AC ABJ04479;
 XX
 XX 24-OCT-2002 (first entry)
 DT HUVEC cell targeting peptide 26.
 DE
 DE
 XX BRASIL; targeting peptide; bacterial infection;
 KW Biopanning and Rapid Analysis of Selective Interact Ligands; diabetes;
 KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
 KW viral infection; cardiovascular disease; degenerative disease.
 XX
 OS Unidentified.
 XX WO200220822-A2.
 XX
 PD 14-MAR-2002.

XX PF 07-SEP-2001; 2001WO-US028124.
 XX XX
 PR 08-SEP-2000; 2000US-0231266P.
 PR 17-JAN-2000; 2001US-00765101.
 XX XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX XX
 PI Arap W, Pasqualini R;
 XX XX
 DR WPI; 2002-404697/43.
 XX XX
 PT Identification of targeting peptides that can be used to treat diseases
 PT e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis
 PT of Selective Ligands) method comprises a single differential
 PT centrifugation step.
 XX XX
 PS Example 2; Page 64; 167pp; English.
 XX XX
 CC The invention comprises a method (BRASIL - Biopanning and Rapid Analysis
 CC of Selective Interactive Ligands) to obtain a targeting peptide. The
 CC BRASIL method of the invention involves: exposing a target to a phage
 CC display library in a first phase; exposing the first phase to a second
 CC phase, and separating the phage bound to the target from unbound phage.
 CC The BRASIL method of the invention allows cell phages to be separated
 CC from the remaining unbound phage in a single differential centrifugation
 CC step. When compared to conventional cell panning methods, the BRASIL
 CC method shows a significant increase in recovery of specific phage and a
 CC substantial decrease in background. The BRASIL method is useful for
 CC identifying targeting peptides. The targeting peptides identified by the
 CC method of the invention are useful for treating disease states, such as:
 CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune
 CC disease; bacterial infection; viral infection; cardiovascular disease and
 CC degenerative disease. The present amino acid sequence represents a
 CC targeting peptide of the invention
 XX XX
 SQ Sequence 8 AA;
 Query Match 58.8%; Score 30; DB 5; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CLHRGNCS 8
 | : : : :
 Db 1 CSYKANSC 8
 | : : : :
 RESULT 8
 AAY48662
 ID AAY48662 standard; peptide; 8 AA.
 XX XX
 AC AAY48662;
 XX XX
 DT 20-MAR-2003 (revised)
 DT 10-DEC-1999 (first entry)
 XX XX
 DE Membrane dipeptidase-binding lung homing peptide #33.
 XX XX
 KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
 KW membrane dipeptidase.
 XX XX
 OS Synthetic.
 OS Homo sapiens.
 XX XX
 PN WO9946284-A2.
 XX XX
 PD 16-SEP-1999.
 XX XX
 PF 10-MAR-1999; 99WO-US005284.
 XX XX
 PR 13-MAR-1998; 98US-00042107.
 PR 26-FEB-1999; 99US-00258754.
 XX XX
 PA (BURN-) BURNHAM INST.
 XX XX
 PI Rajotte D, Pasqualini R, Ruoslahti EI;
 XX XX
 DR WPI; 1999-571717/48.
 XX XX
 PT New peptides which selectively home to organs or tissues, used for, e.g.
 PT identifying target ligands and for therapy of pathological conditions.
 XX XX
 PS Claim 27; Page 150; 193pp; English.
 XX XX
 CC The present invention describes peptides that selectively home to a
 CC tissue or organ. The peptides can be used for identifying an organ or
 CC tissue for, e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis
 CC of Selective Ligands) method comprises a single differential
 CC centrifugation step.
 XX XX
 PS Example 2; Page 64; 167pp; English.
 XX XX
 CC The invention comprises a method (BRASIL - Biopanning and Rapid Analysis
 CC of Selective Interactive Ligands) to obtain a targeting peptide. The
 CC BRASIL method of the invention involves: exposing a target to a phage
 CC display library in a first phase; exposing the first phase to a second
 CC phase, and separating the phage bound to the target from unbound phage.
 CC The BRASIL method of the invention allows cell phages to be separated
 CC from the remaining unbound phage in a single differential centrifugation
 CC step. When compared to conventional cell panning methods, the BRASIL
 CC method shows a significant increase in recovery of specific phage and a
 CC substantial decrease in background. The BRASIL method is useful for
 CC identifying targeting peptides. The targeting peptides identified by the
 CC method of the invention are useful for treating disease states, such as:
 CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune
 CC disease; bacterial infection; viral infection; cardiovascular disease and
 CC degenerative disease. The present amino acid sequence represents a
 CC targeting peptide of the invention
 XX XX
 SQ Sequence 8 AA;
 Query Match 58.8%; Score 30; DB 5; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CLHRGNCS 8
 | : : : :
 Db 1 CSYKANSC 8
 | : : : :
 RESULT 8
 AAY48662
 ID AAY48662 standard; peptide; 8 AA.
 XX XX
 AC AAY48662;
 XX XX
 DT 20-MAR-2003 (revised)
 DT 10-DEC-1999 (first entry)
 XX XX
 DE Membrane dipeptidase-binding lung homing peptide #33.
 XX XX
 KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
 KW membrane dipeptidase.
 XX XX
 OS Synthetic.
 OS Homo sapiens.
 XX XX
 PN WO9946284-A2.
 XX XX
 PD 16-SEP-1999.
 XX XX
 PF 10-MAR-1999; 99WO-US005284.
 XX XX
 PR 13-MAR-1998; 98US-00042107.
 PR 26-FEB-1999; 99US-00258754.
 XX XX
 PA (BURN-) BURNHAM INST.
 XX XX
 PI Rajotte D, Pasqualini R, Ruoslahti EI;
 XX XX
 DR WPI; 1999-571717/48.
 XX XX
 PT New peptides which selectively home to organs or tissues, used for, e.g.
 PT identifying target ligands and for therapy of pathological conditions.
 XX XX
 PS Claim 27; Page 150; 193pp; English.
 XX XX
 CC The present invention describes peptides that selectively home to a
 CC tissue or organ. The peptides can be used for identifying an organ or

XX XX (BURN-) BURNHAM INST.
 XX XX
 PI Rajotte D, Pasqualini R, Ruoslahti EI;
 XX XX
 DR WPI; 1999-571717/48.
 XX XX
 PT New peptides which selectively home to organs or tissues, used for, e.g.
 PT identifying target ligands and for therapy of pathological conditions.
 XX XX
 PS Example 6; Page 144; 193pp; English.
 XX XX
 CC The present invention describes peptides that selectively home to a
 CC tissue or organ. The peptides can be used for identifying an organ or
 CC tissue for, e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis
 CC of Selective Ligands) method comprises a single differential
 CC centrifugation step.
 XX XX
 PS Example 2; Page 64; 167pp; English.
 XX XX
 CC The invention comprises a method (BRASIL - Biopanning and Rapid Analysis
 CC of Selective Interactive Ligands) to obtain a targeting peptide. The
 CC BRASIL method of the invention involves: exposing a target to a phage
 CC display library in a first phase; exposing the first phase to a second
 CC phase, and separating the phage bound to the target from unbound phage.
 CC The BRASIL method of the invention allows cell phages to be separated
 CC from the remaining unbound phage in a single differential centrifugation
 CC step. When compared to conventional cell panning methods, the BRASIL
 CC method shows a significant increase in recovery of specific phage and a
 CC substantial decrease in background. The BRASIL method is useful for
 CC identifying targeting peptides. The targeting peptides identified by the
 CC method of the invention are useful for treating disease states, such as:
 CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune
 CC disease; bacterial infection; viral infection; cardiovascular disease and
 CC degenerative disease. The present amino acid sequence represents a
 CC targeting peptide of the invention
 XX XX
 SQ Sequence 8 AA;
 Query Match 56.9%; Score 29; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CLHRGNCS 8
 | : : : :
 Db 1 CRHESSC 8
 | : : : :
 RESULT 9
 AAY48879
 ID AAY48879 standard; peptide; 8 AA.
 XX XX
 AC AAY48879;
 XX XX
 DT 20-MAR-2003 (revised)
 DT 10-DEC-1999 (first entry)
 XX XX
 DE Membrane dipeptidase-binding retina homing peptide #65.
 XX XX
 KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
 KW membrane dipeptidase.
 XX XX
 OS Synthetic.
 OS Homo sapiens.
 XX XX
 PN WO9946284-A2.
 XX XX
 PD 16-SEP-1999.
 XX XX
 PF 10-MAR-1999; 99WO-US005284.
 XX XX
 PR 13-MAR-1998; 98US-00042107.
 PR 26-FEB-1999; 99US-00258754.
 XX XX
 PA (BURN-) BURNHAM INST.
 XX XX
 PI Rajotte D, Pasqualini R, Ruoslahti EI;
 XX XX
 DR WPI; 1999-571717/48.
 XX XX
 PT New peptides which selectively home to organs or tissues, used for, e.g.
 PT identifying target ligands and for therapy of pathological conditions.
 XX XX
 PS Claim 27; Page 150; 193pp; English.
 XX XX
 CC The present invention describes peptides that selectively home to a
 CC tissue or organ. The peptides can be used for identifying an organ or

CC tissue, for identifying a target molecule expressed by an organ or tissue
 CC or for treating an organ or tissue pathology, where the organ or tissue
 CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,
 CC adrenal gland, liver, and lymph node. The peptide bind to the membrane
 CC dipeptidase (MDP). AA48618 to AA49066 represent sequences which are
 CC used in the exemplification of the present invention. (Updated on 20-MAR-
 CC 2003 to correct PR field.)

XX SQ Sequence 8 AA;

Query Match 54.9%; Score 28; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
 DB 1 CRYKGPSC 8

RESULT 10

ABB98083 ID ABB98083 standard; peptide; 8 AA.

XX AC ABB98083;

XX DT 02-OCT-2002 (first entry)

XX DE Fc effector peptide #9.

XX KW Fc effector; antibody; immunoglobulin; Fc region; binding; vaccine.

XX OS Unidentified.

XX PN WO200244215-A2.

XX PD 06-JUN-2002.

XX PF 30-NOV-2001; 2001WO-GB005301.

XX PR 01-DEC-2000; 2000GB-00029407.

XX PA (COCK/) COCKBAIN J.

XX PA (BREK/) BREKKE O H A.

XX PA (LAUV/) LAUVRAK V.

XX PA (SAND/) SANDLIE I.

XX PI Brekke OHA, Lauvrak V, Sandlie I;

XX DR WPI; 2002-527704/56.

XX PT Binding molecules useful in therapy, diagnosis and imaging, have
 PT polypeptides forming binding sites for target molecules, and Fc effector
 PT peptides displaying functions associated with constant regions of
 PT immunoglobulin heavy chains.

XX PS Claim 10; Page 16; 77pp; English.

XX CC The invention relates to a binding molecule comprising one or more
 CC polypeptides which form a binding site capable of binding a target
 CC molecule, and an Fc effector peptide displaying one or more effector
 CC functions associated with the constant region (Fc) of an immunoglobulin
 CC heavy chain. Peptides of the invention are useful in therapy, diagnosis
 CC or imaging. Therapy using peptides of the invention is likely to be more
 CC effective and less immunogenic than, for example, the targeting of other
 CC therapeutic fusion proteins, as they induce a response based on that
 CC which would be induced by natural intact immunoglobulins in the body. The
 CC Fc effector peptides binds to FcRn receptors that mediate retention of
 CC antibodies in intracellular vesicles in endothelial cells lining blood
 CC vessels in vivo, therefore the binding molecules comprising FcRn-binding
 CC peptides will remain in the body circulation longer than normal antibody
 CC fragments. Peptides of the invention may also be utilised in vaccines.
 CC The current sequence represents a preferred Fc effector peptide of the
 CC invention, which has the ability to bind Fc receptors

XX SQ Sequence 8 AA;

Query Match 54.9%; Score 28; DB 5; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
 DB 1 CLRSGSGC 8

RESULT 11

ABB98084 ID ABB98084 standard; peptide; 8 AA.

XX AC ABB98084;

XX DT 02-OCT-2002 (first entry)

XX DE Fc effector peptide #10.

XX KW Fc effector; antibody; immunoglobulin; Fc region; binding; vaccine.

XX OS Unidentified.

XX PN WO200244215-A2.

XX PD 06-JUN-2002.

XX PF 30-NOV-2001; 2001WO-GB005301.

XX PR 01-DEC-2000; 2000GB-00029407.

XX PA (COCK/) COCKBAIN J.

XX PA (BREK/) BREKKE O H A.

XX PA (LAUV/) LAUVRAK V.

XX PA (SAND/) SANDLIE I.

XX PI Brekke OHA, Lauvrak V, Sandlie I;

XX DR WPI; 2002-527704/56.

XX PT Binding molecules useful in therapy, diagnosis and imaging, have
 PT polypeptides forming binding sites for target molecules, and Fc effector
 PT peptides displaying functions associated with constant regions of
 PT immunoglobulin heavy chains.

XX PS Claim 10; Page 16; 77pp; English.

XX CC The invention relates to a binding molecule comprising one or more
 CC polypeptides which form a binding site capable of binding a target
 CC molecule, and an Fc effector peptide displaying one or more effector
 CC functions associated with the constant region (Fc) of an immunoglobulin
 CC heavy chain. Peptides of the invention are useful in therapy, diagnosis
 CC or imaging. Therapy using peptides of the invention is likely to be more
 CC effective and less immunogenic than, for example, the targeting of other
 CC therapeutic fusion proteins, as they induce a response based on that
 CC which would be induced by natural intact immunoglobulins in the body. The
 CC Fc effector peptides binds to FcRn receptors that mediate retention of
 CC antibodies in intracellular vesicles in endothelial cells lining blood
 CC vessels in vivo, therefore the binding molecules comprising FcRn-binding
 CC peptides will remain in the body circulation longer than normal antibody
 CC fragments. Peptides of the invention may also be utilised in vaccines.
 CC The current sequence represents a preferred Fc effector peptide of the
 CC invention, which has the ability to bind Fc receptors

XX SQ Sequence 8 AA;

Query Match 54.9%; Score 28; DB 5; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
 Db 1 CLRSGRAC 8

RESULT 12
 ABJ04391
 ID ABJ04391 standard; peptide; 8 AA.
 XX
 AC ABJ04391;
 XX
 DT 24-OCT-2002 (first entry)
 XX
 DE HUVEC cell targeting peptide 3.
 XX
 KW BRASIL; targeting peptide; bacterial infection;
 KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
 KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
 KW viral infection; cardiovascular disease; degenerative disease.
 OS Unidentified.
 XX
 PN WO200220822-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 07-SEP-2001; 2001WO-US028124.
 XX
 PR 08-SEP-2000; 2000US-0231266P.
 PR 17-JAN-2001; 2001US-00765101.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Arap W, Pasqualini R;
 XX
 DR WPI; 2002-404697/43.
 XX
 PT Identification of targeting peptides that can be used to treat diseases
 PT e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis
 PT of Selective Ligands) method comprises a single differential
 PT centrifugation step.
 XX
 PS Claim 78; Page 100; 167pp; English.
 XX
 CC The invention comprises a method (BRASIL - Biopanning and Rapid Analysis
 CC of Selective Interactive Ligands) to obtain a targeting peptide. The
 CC BRASIL method of the invention involves: exposing a target to a phage
 CC display library in a first phase; exposing the first phase to a second
 CC phase; and separating the phage bound to the target from unbound phage.
 CC The BRASIL method of the invention allows cell phages to be separated
 CC from the remaining unbound phage in a single differential centrifugation
 CC step. When compared to conventional cell panning methods, the BRASIL
 CC method shows a significant increase in recovery of specific phage and a
 CC substantial decrease in background. The BRASIL method is useful for
 CC identifying targeting peptides. The targeting peptides identified by the
 CC method of the invention are useful for treating disease states, such as:
 CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune
 CC disease; bacterial infection; viral infection; cardiovascular disease and
 CC degenerative disease. The present amino acid sequence represents a
 CC targeting peptide of the invention
 XX
 SQ Sequence 8 AA;

Query Match 52.9%; Score 27; DB 5; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
 Db 1 CLRGKGSVC 8

RESULT 13

ABB98080
 ID ABB98080 standard; peptide; 8 AA.
 XX
 AC ABB98080;
 XX
 DT 02-OCT-2002 (first entry)
 XX
 DE Fc effector peptide #6.
 XX
 KW Fc effector; antibody; immunoglobulin; Fc region; binding; vaccine.
 XX
 OS Unidentified.
 XX
 PN WO200244215-A2.
 XX
 PD 06-JUN-2002.
 XX
 PF 30-NOV-2001; 2001WO-GB005301.
 XX
 PR 01-DEC-2000; 2000GB-00029407.
 XX
 PA (COCK/) COCKBAIN J.
 PA (BREK/) BREKKE O H A.
 PA (LAUV/) LAUVRAK V.
 PA (SAND/) SANDLIE I.
 XX
 PI Brekke OHA, Lauvrak V, Sandlie I;
 XX
 DR WPI; 2002-527704/56.
 XX
 PT Binding molecules useful in therapy, diagnosis and imaging, have
 PT polypeptides forming binding sites for target molecules, and Fc effector
 PT peptides displaying functions associated with constant regions of
 PT immunoglobulin heavy chains.
 XX
 PS Claim 10; Page 16; 77pp; English.
 XX
 CC The invention relates to a binding molecule comprising one or more
 CC polypeptides which form a binding site capable of binding a target
 CC molecule, and an Fc effector peptide displaying one or more effector
 CC functions associated with the constant region (Fc) of an immunoglobulin
 CC heavy chain. Peptides of the invention are useful in therapy, diagnosis
 CC or imaging. Therapy using peptides of the invention is likely to be more
 CC effective and less immunogenic than, for example, the targeting of other
 CC therapeutic fusion proteins, as they induce a response based on that
 CC which would be induced by natural intact immunoglobulins in the body. The
 CC Fc effector peptides binds to FcRn receptors that mediate retention of
 CC antibodies in intracellular vesicles in endothelial cells lining blood
 CC vessels in vivo, therefore the binding molecules comprising FcRn-binding
 CC peptides will remain in the body circulation longer than normal antibody
 CC fragments. Peptides of the invention may also be utilised in vaccines.
 CC The current sequence represents a preferred Fc effector peptide of the
 CC invention, which has the ability to bind Fc receptors
 XX
 SQ Sequence 8 AA;

Query Match 52.9%; Score 27; DB 5; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
 Db 1 CLRSGRGC 8

RESULT 14
 AAW54868
 ID AAW54868 standard; protein; 7 AA.
 XX
 AC AAW54868;
 XX
 DT 11-SEP-1998 (first entry)
 XX

```

DE Homo sapiens Fyb71 peptide.
XX
KW gp-FY protein; Fyb71-81; duffy blood group; antigen; alpha; beta;
KW alternative splicing; RBC; red blood cell; malaria; treatment.
XX
XX Homo sapiens.
XX
XX WO9821224-A1.
XX
XX PD 22-MAY-1998.
XX
XX PF 14-NOV-1997; 97WO-US021067.
XX
XX PR 15-NOV-1996; 96US-00749543.
XX
XX (NYBL-) NEW YORK BLOOD CENT INC.
XX
XX PI Pogo OA, Chaudhuri A;
XX
XX DR WPI; 1998-297854/26.
XX
XX Nucleic acid encoding gp-FY, Duffy antigen proteins - used to prevent
PT vivax malaria and to regulate erythrocyte, neural or renal function.
XX
XX Example 10; Page 27; 87pp; English.
XX
XX The sequence is that of a peptide encoded by Fyb71 which was used in the
CC isolation of gp-FY mRNA
XX
XX Sequence 7 AA;
XX
Query Match 51.0%; Score 26; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLHR 4
   ||||
Db 4 CLHR 7

RESULT 15
AAR96348
ID AAR96348 standard; peptide; 8 AA.
AC AAR96348;
XX
XX 05-JUL-1996 (first entry)
XX
XX RGD cyclic peptide, binds alpha-v,beta3 integrin receptor.
XX
XX RGD-containing peptide; alpha-v, beta-3 integrin receptor; osteoclast;
KW matrix; bone; inhibition; bone resorption; promote; endothelial cell;
KW smooth muscle cell; restenosis; angiogenesis; cyclic.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Disulfide-bond 1. 8
FT Modified-site 1
FT /note= "Acyl-Cys"
FT Modified-site 7
FT /label= OTHER
FT /note= "OTHER = 1,2,3,4-Tetrahydroisoquinoline-3-
FT carboxylic acid"
FT Modified-site 8
FT /note= "Amidated C-terminal"
XX
XX WO9528426-A2.
XX
XX PD 26-OCT-1995.
XX
XX PF 12-APR-1995; 95WO-US004741.
XX

```

```

PR 13-APR-1994; 94US-00227316.
PR 08-SEP-1994; 94US-00303052.
XX
XX (LJOL-) LA JOLLA CANCER RES FOUND.
XX
XX Cheng S, Ingram R, Mullen D, Tschopp J;
XX WPI; 1995-373767/48.
XX
XX Altering alpha-v, beta-3 integrin receptor-mediated binding of cell to
PT matrix - using conformationally restrained peptide of RGD type, e.g. for
PT treating inappropriate angiogenesis or for inhibiting bone resorption.
XX
XX Claim 84; Page 78; 99pp; English.
XX
XX The sequences given in AAR96301-417 are non-naturally occurring RGD-
CC containing peptides which alter the alpha-v, beta-3 integrin receptor
CC binding of a cell to a matrix, such as the binding of an osteoclast to a
CC matrix such as bone. These peptides inhibit bone resorption and can
CC inhibit or promote alpha-v, beta-3-mediated cell attachment depending on
CC whether they are present in the cell in a soluble form or are bound to a
CC solid substrate. These peptides can be used in the amelioration of the
CC severity of a pathology involving alpha-v, beta-3 receptor-mediated
CC binding of a cell, such as an osteoclast, endothelial cell or smooth
CC muscle cell to a matrix. They are used for treating conditions associated
CC with restenosis or inappropriate or insufficient angiogenesis, or for
CC inhibiting osteoclast binding to the matrix
XX
XX Sequence 8 AA;
XX
Query Match 51.0%; Score 26; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
   ||||
Db 1 CAARGTXC 8

Search completed: August 3, 2005, 12:16:47
Job time : 163 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 12:09:38 ; Search time 41 Seconds
(without alignments)
14.566 Million cell updates/sec

Title: US-09-910-582B-9
Perfect score: 51
Sequence: 1 CLHRGNSC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 77247

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	8	3	US-09-326-718-9
2	31	60.8	8	3	US-09-187-859-2736
3	31	60.8	8	4	US-09-839-542B-2736
4	30	58.8	8	3	US-09-258-754-240
5	30	58.8	8	3	US-09-042-107-240
6	30	58.8	8	3	US-09-187-859-1084
7	30	58.8	8	4	US-09-839-542B-1084
8	30	58.8	8	4	US-09-722-250D-240
9	30	58.8	8	4	US-09-676-475A-240
10	29	56.9	8	3	US-09-258-754-33
11	29	56.9	8	3	US-09-042-107-33
12	29	56.9	8	4	US-09-722-250D-33
13	29	56.9	8	4	US-09-676-475A-33
14	28	54.9	8	3	US-09-258-754-257
15	28	54.9	8	3	US-09-042-107-257
16	28	54.9	8	4	US-09-722-250D-257
17	28	54.9	8	4	US-09-676-475A-257
18	26	51.0	7	2	US-08-749-526-12
19	26	51.0	8	1	US-08-526-710-4
20	26	51.0	8	2	US-08-421-695A-125
21	26	51.0	8	3	US-08-862-855-4
22	26	51.0	8	3	US-09-226-985-4
23	26	51.0	8	3	US-09-227-906-4
24	26	51.0	8	3	US-09-187-859-3086
25	26	51.0	8	4	US-09-839-542B-3086
26	26	51.0	8	4	US-09-535-852-430
27	26	51.0	8	4	US-09-428-082B-1091

ALIGNMENTS

RESULT 1

US-09-326-718-9
; Sequence 9, Application US/09326718
; Patent No. 6303573
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: MacKenna, Deidre A.
; TITLE OF INVENTION: Heart Homing Peptides and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-LJ 3512
; CURRENT APPLICATION NUMBER: US/09/326,718
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-326-718-9

Query Match 100.0%; Score 51; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
|:|:|:|:|
DB 1 CLHRGNSC 8

RESULT 2

US-09-187-859-2736
; Sequence 2736, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2736
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-187-859-2736

Query Match 60.8%; Score 31; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
|:|:|:|
DB 1 CINRDNGC 8

RESULT 3

US-09-839-542B-2736
; Sequence 2736, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2736
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-839-542B-2736

Query Match 60.8%; Score 31; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
|:|:|:|
DB 1 CINRDNGC 8

RESULT 4

US-09-258-754-240
; Sequence 240, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-240

Query Match 58.8%; Score 30; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
|:|:|:|
DB 1 CMSLGNCC 8

RESULT 5

US-09-042-107-240
; Sequence 240, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107

; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-240

Query Match 58.8%; Score 30; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
|: |||
Db 1 CMSGNGC 8

RESULT 6
US-09-187-859-1084
; Sequence 1084, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187.859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1084
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-09-187-859-1084

Query Match 58.8%; Score 30; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
|: |||
Db 1 CMSGNGC 8

RESULT 7
US-09-839-542B-1084
; Sequence 1084, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839.542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1084
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on

; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-09-839-542B-1084

Query Match 58.8%; Score 30; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
|: |||
Db 1 CMSGNGC 8

RESULT 8
US-09-722-250D-240
; Sequence 240, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722.250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042.107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-240

Query Match 58.8%; Score 30; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
|: |||
Db 1 CMSGNGC 8

RESULT 9
US-09-676-475A-240
; Sequence 240, Application US/09676475A
; Patent No. 6784153
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LA 4377
; CURRENT APPLICATION NUMBER: US/09/676.475A
; CURRENT FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 09/042.107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-676-475A-240

Query Match 58.8%; Score 30; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 CLHRGNSC 8
Db 1 CMSGNMC 8

RESULT 10
US-09-258-754-33
; Sequence 33, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-33

Query Match 56.9%; Score 29; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
Db 1 CRHESSC 8

RESULT 13
US-09-676-475A-33
; Sequence 33, Application US/09676475A
; Patent No. 6784153
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LA 4377
; CURRENT APPLICATION NUMBER: US/09/676,475A
; CURRENT FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-676-475A-33

Query Match 56.9%; Score 29; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
Db 1 CRHESSC 8

RESULT 14
US-09-258-754-257
; Sequence 257, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-257-33

Query Match 56.9%; Score 29; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
Db 1 CRHESSC 8

RESULT 11
US-09-042-107-33
; Sequence 33, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-33

Query Match 56.9%; Score 29; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
Db 1 CRHESSC 8

RESULT 12
US-09-722-250D-33
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; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-257

Query Match 54.9%; Score 28; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNCS 8
|.:|:|
Db 1 CRYKGPSC 8

RESULT 15
US-09-042-107-257
; Sequence 257, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-257

Query Match 54.9%; Score 28; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNCS 8
|.:|:|
Db 1 CRYKGPSC 8

Search completed: August 3, 2005, 12:21:13
Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 12:19:48 ; Search time 150 Seconds
(without alignments)
20.779 Million cell updates/sec

Title: US-09-910-582B-9
Perfect score: 51
Sequence: 1 CLHRGNSC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 99867

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA:*

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	51	100.0	8	9	US-09-782-650-4
2	51	100.0	8	10	US-09-910-582B-9
3	51	100.0	8	17	US-10-838-289-37
4	31	60.8	8	14	US-10-006-869-2736
5	31	60.8	8	15	US-10-395-032-2736
6	30	58.8	8	14	US-10-006-869-1084
7	30	58.8	8	15	US-10-395-032-1084
8	30	58.8	8	15	US-10-363-208-97
9	30	58.8	8	17	US-10-838-289-297
10	30	58.8	8	17	US-10-363-205-130
11	30	58.8	8	17	US-10-607-595-240
12	45.1	45.1	6	16	US-10-865-661-1

29	56.9	8	17	US-10-838-289-136	Sequence 136, App
28	56.9	8	17	US-10-607-595-33	Sequence 33, Appl
28	54.9	8	16	US-10-433-452A-9	Sequence 9, Appl
28	54.9	8	16	US-10-433-452A-10	Sequence 10, Appl
28	54.9	8	17	US-10-838-289-314	Sequence 314, App
28	54.9	8	17	US-10-607-595-257	Sequence 257, App
28	54.9	8	17	US-10-923-940-10	Sequence 10, Appl
28	54.9	8	16	US-10-433-452A-6	Sequence 6, Appl
27	52.9	8	16	US-10-469-131-25	Sequence 42, Appl
27	52.9	8	17	US-10-363-205-42	Sequence 25, Appl
27	52.9	8	17	US-10-923-940-8	Sequence 8, Appl
27	52.9	8	17	US-10-923-940-9	Sequence 9, Appl
27	52.9	8	17	US-10-923-940-11	Sequence 11, Appl
26	51.0	8	11	US-09-922-227-4	Sequence 4, Appl
26	51.0	8	14	US-10-006-869-3086	Sequence 3086, Ap
26	51.0	8	15	US-10-395-032-3086	Sequence 3086, Ap
26	51.0	8	15	US-10-464-302-52	Sequence 52, Appl
26	51.0	8	15	US-10-609-217-1091	Sequence 1091, Ap
26	51.0	8	15	US-10-363-208-67	Sequence 67, Appl
26	51.0	8	15	US-10-363-208-111	Sequence 111, App
26	51.0	8	15	US-10-632-388-1091	Sequence 1091, Ap
26	51.0	8	15	US-10-651-723-1091	Sequence 1091, Ap
26	51.0	8	15	US-10-645-761-1091	Sequence 1091, Ap
26	51.0	8	15	US-10-666-696-1091	Sequence 1091, Ap
26	51.0	8	15	US-10-653-048-1091	Sequence 1091, Ap
26	51.0	8	16	US-10-433-452A-5	Sequence 5, Appl
26	51.0	8	16	US-10-433-452A-11	Sequence 11, Appl
26	51.0	8	16	US-10-433-452A-56	Sequence 56, Appl
26	51.0	8	16	US-10-654-578-430	Sequence 430, App
26	51.0	8	17	US-10-943-372-4	Sequence 4, Appl
26	51.0	8	17	US-10-838-289-2	Sequence 2, Appl
26	51.0	8	18	US-10-645-784-1091	Sequence 1091, Ap
25	49.0	8	9	US-09-234-395-307	Sequence 307, App
25	49.0	8	9	US-09-305-928-307	Sequence 307, App
25	49.0	8	9	US-09-769-145-42	Sequence 42, Appl
25	49.0	8	13	US-10-006-982-18	Sequence 18, Appl
25	49.0	8	14	US-10-105-008-42	Sequence 42, Appl
25	49.0	8	14	US-10-006-869-3653	Sequence 3653, Ap
25	49.0	8	14	US-10-058-821-27	Sequence 27, Appl
25	49.0	8	15	US-10-359-546-28	Sequence 28, Appl
25	49.0	8	15	US-10-395-032-3553	Sequence 3553, Ap
25	49.0	8	15	US-10-425-557-42	Sequence 42, Appl
25	49.0	8	15	US-10-363-208-98	Sequence 98, Appl
25	49.0	8	15	US-10-412-701-42	Sequence 42, Appl
25	49.0	8	16	US-10-433-452A-8	Sequence 8, Appl
25	49.0	8	16	US-10-632-678-42	Sequence 42, Appl
25	49.0	8	16	US-10-654-578-938	Sequence 938, App
25	49.0	8	16	US-10-759-379-307	Sequence 307, App
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24	47.1	8	11	US-09-922-227-25	Sequence 25, Appl
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24	47.1	8	13	US-10-006-982-19	Sequence 19, Appl
24	47.1	8	14	US-10-105-008-43	Sequence 43, Appl
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24	47.1	8	14	US-10-006-869-3359	Sequence 3359, Ap
24	47.1	8	15	US-10-359-546-51	Sequence 51, Appl
24	47.1	8	15	US-10-395-032-3101	Sequence 3101, Ap
24	47.1	8	15	US-10-395-032-3359	Sequence 3359, Ap
24	47.1	8	15	US-10-425-557-43	Sequence 43, Appl
24	47.1	8	15	US-10-363-208-81	Sequence 81, Appl
24	47.1	8	15	US-10-412-701-43	Sequence 43, Appl
24	47.1	8	16	US-10-433-452A-7	Sequence 7, Appl
24	47.1	8	16	US-10-632-678-43	Sequence 43, Appl
24	47.1	8	16	US-10-654-578-445	Sequence 445, App
24	47.1	8	16	US-10-654-578-703	Sequence 703, App
24	47.1	8	17	US-10-943-372-26	Sequence 25, Appl
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24	47.1	8	17	US-10-838-289-23	Sequence 23, Appl
24	47.1	8	17	US-10-838-289-24	Sequence 24, Appl
24	47.1	8	17	US-10-838-289-315	Sequence 315, App
24	47.1	8	17	US-10-607-595-258	Sequence 258, App
23	45.1	6	16	US-10-865-661-1	Sequence 1, Appl

85 23 45.1 7 18 US-10-755-415-355 Sequence 355, App
86 23 45.1 8 11 US-09-896-784-31 Sequence 31, Appl
87 23 45.1 8 14 US-10-215-168-9 Sequence 9, Appl
88 23 45.1 8 14 US-10-006-869-3347 Sequence 3347, Ap
89 23 45.1 8 15 US-10-395-032-3347 Sequence 3347, Ap
90 23 45.1 8 16 US-10-433-452A-12 Sequence 12, Appl
91 23 45.1 8 16 US-10-363-204-241 Sequence 241, App
92 23 45.1 8 16 US-10-654-578-691 Sequence 691, App
93 23 45.1 8 17 US-10-838-289-145 Sequence 145, App
94 23 45.1 8 17 US-10-607-595-40 Sequence 40, Appl
95 23 45.1 8 17 US-10-488-779A-44 Sequence 44, Appl
96 22.5 44.1 7 14 US-10-006-869-3085 Sequence 3085, Ap
97 22.5 44.1 7 15 US-10-395-032-3085 Sequence 3085, Ap
98 22.5 44.1 7 16 US-10-654-578-429 Sequence 429, App
99 22 43.1 6 9 US-09-821-831-41 Sequence 41, Appl
100 22 43.1 6 17 US-10-921-065-41 Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-09-782-650-4
; Sequence 4, Application US/09782650
; Patent No. US2002001950A1
; GENERAL INFORMATION:
; APPLICANT: Levine, Arnold J.
; APPLICANT: Mitterer, Artur
; APPLICANT: Falkner, Falko-Guenter
; APPLICANT: Scheiflinger, Friedrich
; APPLICANT: Dörner, Friedrich
; APPLICANT: Edwards LifeSciences Corporation
; TITLE OF INVENTION: Targeted Angiogenesis
; FILE REFERENCE: 20553D-000611US
; CURRENT APPLICATION NUMBER: US/09/782,650
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: US 09/324,079
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 09/327,045
; PRIOR FILING DATE: 1999-06-07
; PRIOR APPLICATION NUMBER: PCT/US00/14988
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:targeting
US-09-782-650-4

Query Match 100.0%; Score 51; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
| | | | | | | |
Db 1 CLHRGNSC 8

RESULT 2
US-09-910-582B-9
; Sequence 9, Application US/09910582B
; Publication No. US20030045476A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Mackenna, Deirdre A.
; TITLE OF INVENTION: Heart Homing Conjugates
; FILE REFERENCE: P-LJ 4857
; CURRENT APPLICATION NUMBER: US/09/910,582B
; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 09/326,718
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-910-582B-9

Query Match 100.0%; Score 51; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
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Db 1 CLHRGNSC 8

RESULT 3
US-10-838-289-37
; Sequence 37, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jimming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; TITLE OF INVENTION: NANOSHELLS
; FILE REFERENCE: CMRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Heart homing peptide
US-10-838-289-37

Query Match 100.0%; Score 51; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
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Db 1 CLHRGNSC 8

RESULT 4
US-10-006-869-2736
; Sequence 2736, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2736
; LENGTH: 8

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-10-006-869-2736

Query Match 60.8%; Score 31; DB 14; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
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Db 1 C1NRDNGC 8

RESULT 5
US-10-395-032-2736
; Sequence 2736, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2736
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-10-395-032-2736

Query Match 60.8%; Score 31; DB 15; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
|:|:|
Db 1 C1NRDNGC 8

RESULT 6
US-10-006-869-1084
; Sequence 1084, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1084
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-10-006-869-1084

Query Match 58.8%; Score 30; DB 14; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
|:|:|
Db 1 C1DSGNGC 8

RESULT 7
US-10-395-032-1084
; Sequence 1084, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1084
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-10-395-032-1084

Query Match 58.8%; Score 30; DB 15; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
|:|:|
Db 1 C1DSGNGC 8

RESULT 8
US-10-363-208-97
; Sequence 97, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(8)
; OTHER INFORMATION: synthetic construct
US-10-363-208-97

Query Match 58.8%; Score 30; DB 15; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
|:|:|:|
Db 1 C1WRGSGC 8

RESULT 9
US-10-838-289-297
; Sequence 297, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jinming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; TITLE OF INVENTION: NANOSHHELLS
; FILE REFERENCE: CWRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 297
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Retina homing peptide
US-10-838-289-297

Query Match 58.8%; Score 30; DB 17; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNCS 8
| : ||:|
Db 1 CMSLGNCS 8

RESULT 10
US-10-363-205-130
; Sequence 130, Application US/10363205
; Publication No. US20050074747A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Biopanning and Rapid Analysis of Selective Interactive Ligands (B
; FILE REFERENCE: 005774.P004PCT
; CURRENT APPLICATION NUMBER: US/10/363,205
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(8)
; OTHER INFORMATION: synthetic construct
US-10-363-205-130

Query Match 58.8%; Score 30; DB 17; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNCS 8
| : ||:|
Db 1 CSYKANS 8

RESULT 11
US-10-607-595-240
; Sequence 240, Application US/10607595
; Publication No. US20050074812A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata

; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/10/607,595
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/722,250
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-607-595-240

Query Match 58.8%; Score 30; DB 17; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNCS 8
| : ||:|
Db 1 CMSLGNCS 8

RESULT 12
US-10-838-289-136
; Sequence 136, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jinming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; TITLE OF INVENTION: NANOSHHELLS
; FILE REFERENCE: CWRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Lung homing peptide
US-10-838-289-136

Query Match 56.9%; Score 29; DB 17; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CLHRGNCS 8
| : ||:|
Db 1 CRHSSSC 8

RESULT 13
US-10-607-595-33
; Sequence 33, Application US/10607595
; Publication No. US20050074812A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514

; CURRENT APPLICATION NUMBER: US/10/607,595
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/722,250
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-607-595-33

Query Match 56.9%; Score 29; DB 17; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
|||:|
Db 1 CRHSSC 8

RESULT 14
US-10-433-452A-9
; Sequence 9, Application US/10433452A
; Publication No. US20040101905A1
; GENERAL INFORMATION:
; APPLICANT: Brekke, Ole Henrik
; APPLICANT: Lauvrak, Vigdis
; APPLICANT: Sandlie, Inger
; TITLE OF INVENTION: Hybrid Antibodies
; FILE REFERENCE: DEH-0014
; CURRENT APPLICATION NUMBER: US/10/433,452A
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: GB 0029407.4
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fc effector peptide
US-10-433-452A-9

Query Match 54.9%; Score 28; DB 16; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
|||:|
Db 1 CLRSGSC 8

RESULT 15
US-10-433-452A-10
; Sequence 10, Application US/10433452A
; Publication No. US20040101905A1
; GENERAL INFORMATION:
; APPLICANT: Brekke, Ole Henrik
; APPLICANT: Lauvrak, Vigdis
; APPLICANT: Sandlie, Inger
; TITLE OF INVENTION: Hybrid Antibodies
; FILE REFERENCE: DEH-0014
; CURRENT APPLICATION NUMBER: US/10/433,452A
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: GB 0029407.4
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fc effector peptide
US-10-433-452A-10

Query Match 54.9%; Score 28; DB 16; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
|||:|
Db 1 CLRSGSC 8

Search completed: August 3, 2005, 12:32:58
Job time : 151 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 12:29:24 ; Search time 38 Seconds
(without alignments)
30.384 Million cell updates/sec

Title: US-09-910-582B-10
Perfect score: 74
Sequence: 1 CRSWNKADNRSC 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

PIR 79: *
1: piri: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	33.8	10	2 PH0923	T-cell receptor be
2	22	29.7	5	2 JH0253	gut pentapeptide -
3	20	27.0	11	2 S32575	ribosomal protein
4	20	27.0	12	2 S51737	T-cell receptor be
5	20	27.0	12	2 B49033	T-cell receptor de
6	19	25.7	8	2 S19288	acylase - Kluyvera
7	19	25.7	10	2 A35556	hypothetical prote
8	19	25.7	10	2 S23370	T-cell receptor al
9	19	25.7	10	2 F49033	T-cell receptor ga
10	19	25.7	10	2 C41946	T-cell receptor ga
11	19	25.7	11	2 PH1376	T antigen variant
12	19	25.7	12	2 S36902	Em protein - wheat
13	18	24.3	8	2 S59822	metallothionein is
14	18	24.3	8	2 C61512	variant surface gl
15	18	24.3	8	2 I57018	gene Cfr protein
16	18	24.3	9	2 PT0272	Ig heavy chain CRD
17	18	24.3	11	2 I41946	T-cell receptor ga
18	18	24.3	11	2 PH0903	T-cell receptor be
19	17	23.0	6	2 F41946	T-cell receptor ga
20	17	23.0	8	2 S70727	ipgf protein - Shi
21	17	23.0	8	2 A38887	T-cell receptor ga
22	17	23.0	8	2 A39308	glycine reductase
23	17	23.0	8	2 A41117	acetylcholinestera
24	17	23.0	10	2 JCI367	thyroliberin poten
25	17	23.0	10	2 B49033	T-cell receptor ga
26	17	23.0	10	2 D41946	T-cell receptor ga
27	17	23.0	11	2 D41946	T-cell receptor ga
28	17	23.0	11	2 B41946	T-cell receptor ga
29	17	23.0	11	2 C38887	T-cell receptor ga

30	17	23.0	11	2 A49037	TCR gamma V-J regi
31	17	23.0	11	2 B49037	TCR gamma V-J regi
32	17	23.0	11	2 C49037	TCR gamma V-J regi
33	17	23.0	11	2 S45698	gamma-MSH-like pro
34	17	23.0	12	2 PH1308	Ig heavy chain DJ
35	17	23.0	12	2 S25039	Ig heavy chain V r
36	16	21.6	5	2 PT0580	T-cell receptor be
37	16	21.6	7	4 I55382	hypothetical pepti
38	16	21.6	9	2 PT0299	Ig heavy chain CRD
39	16	21.6	9	2 PH0943	T-cell receptor be
40	16	21.6	10	2 S15118	dihydrofolate redu
41	16	21.6	10	2 S63696	DNA polymerase - y
42	16	21.6	10	2 PT0310	Ig heavy chain CRD
43	16	21.6	10	2 PH0807	T-cell receptor al
44	16	21.6	11	2 A34662	Achatina cardio-ex
45	16	21.6	11	2 S05002	corazonin - Americ
46	16	21.6	12	2 S26548	T-cell receptor be
47	16	21.6	12	2 S26553	T-cell receptor be
48	16	21.6	12	2 A49033	T-cell receptor de
49	15	20.3	4	2 PT0661	T-cell receptor be
50	15	20.3	5	2 PT0695	T-cell receptor be
51	15	20.3	6	2 A31263	dihydrofolate redu
52	15	20.3	6	2 B35840	cerebellar degener
53	15	20.3	6	2 A61068	locustakinin - mig
54	15	20.3	7	2 S38516	mablin II chain
55	15	20.3	7	2 PN0649	pullulanase (EC 3.
56	15	20.3	7	2 S57274	triacylglycerol li
57	15	20.3	7	2 A61081	tryptophyllin, bas
58	15	20.3	8	2 S10596	adipokinetic hormo
59	15	20.3	8	2 JS0315	leucokinin V - Mad
60	15	20.3	8	2 JS0316	leucokinin VI - Ma
61	15	20.3	8	2 JS0317	leucokinin VII - M
62	15	20.3	8	2 JS0318	leucokinin VIII -
63	15	20.3	8	2 A28495	conopressin G - co
64	15	20.3	9	2 B28495	conopressin S - co
65	15	20.3	9	2 A24244	adipokinetic hormo
66	15	20.3	9	2 JS0302	xenopsin-related p
67	15	20.3	9	2 A60320	xenopsin-related p
68	15	20.3	9	2 I58350	gene c-mpl protein
69	15	20.3	9	2 PH0921	T-cell receptor be
70	15	20.3	9	2 S39040	lysine-conopressin
71	15	20.3	9	2 PC2021	oxytocin-related p
72	15	20.3	9	2 D57444	neuropeptide Grb-A
73	15	20.3	9	2 B45020	probable minipolyp
74	15	20.3	10	2 C39191	hypothetical prote
75	15	20.3	10	2 PT0322	Ig heavy chain CRD
76	15	20.3	10	2 B38887	T-cell receptor ga
77	15	20.3	10	2 A59272	peptide-N4-(N-acet
78	15	20.3	10	2 H37196	bradykinin-potenti
79	15	20.3	10	2 S53789	neuropeptide Pec-H
80	15	20.3	11	2 S66196	alcohol dehydrogen
81	15	20.3	11	2 S04875	mfs protein - Bra
82	15	20.3	11	2 S70338	napin small chain
83	15	20.3	11	2 S68637	acetylcholinestera
84	15	20.3	12	2 PH1675	Ig heavy chain V r
85	15	20.3	12	2 PT0274	Ig heavy chain CRD
86	15	20.3	12	2 PH1324	Ig heavy chain DJ
87	15	20.3	12	2 H41946	T-cell receptor ga
88	15	20.3	12	2 I41235	glutamine-tRNA lig
89	15	20.3	12	2 S29859	gene p10 protein -
90	15	20.3	12	2 I77529	estrogen receptor
91	14	18.9	7	2 PT0576	T-cell receptor be
92	14	18.9	8	2 A37521	R-phycocerythrin ga
93	14	18.9	9	2 S78426	S2.5K protein - sp
94	14	18.9	10	2 A40753	aldehyde ferredoxi
95	14	18.9	11	2 B43669	hypothetical prote
96	14	18.9	11	2 T06383	hypothetical prote
97	14	18.9	11	2 PT0249	Ig heavy chain CRD
98	14	18.9	11	2 PH1375	T antigen variant
99	14	18.9	11	2 PQ0731	unidentified 5.7/3
100	14	18.9	11	2 S23926	major glycoprotein

ALIGNMENTS

RESULT 1
PH0923
T-cell receptor beta chain V-D-J region (isolate 9) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0923
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A;Reference number: PH0991; MUID:92078857; PMID:1836012
A;Accession: PH0923
A;Molecule type: mRNA
A;Residues: 1-10 <GO>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

Query Match 33.8%; Score 25; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRSWNK 6
| | | :
Db 1 CASNGR 6

RESULT 2
JH0253
gut pentapeptide - Japanese eel
C;Species: Anguilla japonica (Japanese eel)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C;Accession: JH0253
R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A;Reference number: JH0253; MUID:92062113; PMID:1953755
A;Accession: JH0253
A;Molecule type: protein
A;Residues: 1-5 <UES>
A;Experimental source: gut
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric
, and of the circular muscle of the gastro-intestinal junction.

Query Match 29.7%; Score 22; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 WNK 6
| | | :
Db 3 WNK 5

RESULT 3
S32575
ribosomal protein S2, plastid - squawroot plastid (fragment)
C;Species: plastid Conopholis americana (squawroot)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S32575
R;Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; dePamphilis, C.W.; Palmer, J.D.
Curr. Genet. 20, 515-518, 1991
A;Title: Lack of a functional plastid tRNA(Cys) gene is associated with loss of photosyn
A;Reference number: S32575; MUID:92145776; PMID:1723664
A;Accession: S32575
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <TAY>
A;Cross-references: UNIPROT:P42341; EMBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276
C;Genetics:
A;Gene: rps2
A;Genome: plastid
C;Superfamily: Escherichia coli ribosomal protein S2

C;Keywords: plastid; protein biosynthesis; ribosome

Query Match 27.0%; Score 20; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.9e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RSWN 5
| | | :
Db 4 RYWN 7

RESULT 4
S51737
T-cell receptor beta-chain joining region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
C;Accession: S51737
R;Durinovic-Bello, I.; Steinle, A.; Ziegler, A.G.; Schendel, D.J.
submitted to the EMBL Data Library, November 1993
A;Reference number: S51732
A;Accession: S51737
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <DUR>
A;Cross-references: EMBL:Z28345; NID:g607126; PIDN:CAA82199.1; PID:g607127
C;Keywords: T-cell receptor

Query Match 27.0%; Score 20; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.1e+03; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRSWNKAD 8
| | | :
Db 1 CASSQSEAD 8

RESULT 5
B49033
T-cell receptor delta chain V-D-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: B49033
R;Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.
Eur. J. Immunol. 21, 2999-3007, 1991
A;Title: Functionally distinct subsets of human gamma/delta T cells.
A;Reference number: A49033; MUID:92083926; PMID:1684157
A;Accession: B49033
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-12 <MOR>
A;Cross-references: GB:S72580; NID:g240692; PIDN:AAB20628.1; PID:g240693
A;Note: sequence extracted from NCBI backbone (NCBIN:72580, NCBI:P:72582)
C;Keywords: T-cell receptor

Query Match 27.0%; Score 20; DB 2; Length 12;
Best Local Similarity 28.6%; Pred. No. 3.1e+03; Indels 0; Gaps 0;
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRSWNKA 7
| | | :
Db 3 CDTWGSS 9

RESULT 6
S19288
acylase - Kluyvera cryocrescens
C;Species: Kluyvera cryocrescens
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S19288
R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.
Biochem. J. 280, 659-662, 1991
A;Title: Chemical modification of serine at the active site of penicillin acylase from Kl
A;Reference number: S19288; MUID:92109664; PMID:1764029

A;Accession: S19288
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <MAR>
A;Cross-references: UNIPROT:Q7M124

Query Match 25.7%; Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRSW 4
| : |
Db 1 CNMW 4

RESULT 7

A35556
hypothetical protein (ODC region) - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 30-Sep-1993
C;Accession: A35556
R;Moshier, J.A.; Gilbert, J.D.; Skunca, M.; Donescu, J.; Almodovar, K.M.; Luk, G.D.
J. Biol. Chem. 265, 4884-4892, 1990
A;Title: Isolation and expression of a human ornithine decarboxylase gene.
A;Reference number: A35556; MUID:90202959; PMID:2318872
A;Accession: A35556
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-10 <MOS>
A;Cross-references: GB:J05271

Query Match 25.7%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRSW 4
| : |
Db 5 CGAW 8

RESULT 8

S23370
T-cell receptor alpha chain J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S23370
R;Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichman
Eur. J. Immunol. 21, 2749-2754, 1991
A;Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheu
A;Reference number: S23364; MUID:92037820; PMID:1657615
A;Accession: S23370
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-10 <PLU>
A;Cross-references: EMBL:X58165
C;Keywords: T-cell receptor

Query Match 25.7%; Score 19; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.8e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WNKADR 10
| : |
Db 3 WDNDMR 9

RESULT 9

F49033
T-cell receptor gamma chain V-D-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: F49033
R;Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.

Eur. J. Immunol. 21, 2999-3007, 1991
A;Title: Functionally distinct subsets of human gamma/delta T cells.
A;Reference number: A49033; MUID:92083926; PMID:1684157
A;Accession: F49033
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-10 <MOR>

A;Cross-references: GB:S72605; NID:G240700; PIDN:AAB20632.1; PID:G240701
A;Note: sequence extracted from NCBI backbone (NCBIN:72605, NCBIPI:72606)
C;Keywords: T-cell receptor

Query Match 25.7%; Score 19; DB 2; Length 10;
Best Local Similarity 33.3%; Pred. No. 3.8e+03;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRSW 6
| : |
Db 1 CALWER 6

RESULT 10

C41946
T-cell receptor gamma chain (it.60) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: C41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: C41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-10 <WHE>
C;Keywords: T-cell receptor

Query Match 25.7%; Score 19; DB 2; Length 10;
Best Local Similarity 28.6%; Pred. No. 3.8e+03;
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRSW 7
| : |
Db 2 CAVWSS 8

RESULT 11

PH1376
T antigen variant K-3 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C;Accession: PH1376
R;Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.
J. Exp. Med. 176, 449-457, 1992
A;Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for tra
A;Reference number: PH1373; MUID:92364547; PMID:1380062
A;Accession: PH1376
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-11 <Lil>

Query Match 25.7%; Score 19; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRSW 6
| : |
Db 1 CKGVNK 6

RESULT 12

S36902
Em protein - wheat (fragment)
C;Species: Triticum sp. (wheat)

C;Date: 04-Mar-1994 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004

C;Accession: S36902
 R;Taylor, R.M.; Cumming, A.C.
 FEBS Lett. 331, 76-80, 1993
 A;Title: Purification of an endoproteinase that digests the wheat 'Em' protein in vitro,
 A;Reference number: S36902; MUID:94009650; PMID:8405415
 A;Accession: S36902
 A;Molecule type: protein
 A;Residues: 1-12 <TAY>
 A;Cross-references: UNIPROT:Q7M272
 C;Superfamily: embryonic abundant protein Em

Query Match 25.78; Score 19; DB 2; Length 12;
 Best Local Similarity 57.13; Pred. No. 4.5e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 NKADNRS 11
 | | | |
 Db 4 NLAEGRS 10

RESULT 13

S59622
 metallothionein isoform a, cadmium-binding - Ariantha arbustorum (terrestrial snail) (fra
 C;Species: Ariantha arbustorum
 C;Date: 19-Mar-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
 R;Berger, B.; Hunziker, P.E.; Hauer, C.R.; Birchler, N.; Dallinger, R.
 Biochem. J. 311, 951-957, 1995
 A;Title: Mass spectrometry and amino acid sequencing of two cadmium-binding metallothion
 A;Reference number: S59621; MUID:96067616; PMID:7487956
 A;Accession: S59622
 A;Molecule type: protein
 A;Residues: 1-8 <BER>
 A;Cross-references: UNIPROT:P55946
 C;Superfamily: metallothionein
 C;Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 24.3%; Score 18; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 NRSC 12
 | | | |
 Db 2 NSSC 5

RESULT 14

C61512
 variant surface glycoprotein MITat 1.4 - Trypanosoma brucei (fragment)
 C;Species: Trypanosoma brucei
 C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
 C;Accession: C61512
 R;Holder, A.A.; Cross, G.A.M.
 Mol. Biochem. Parasitol. 2, 135-150, 1981
 A;Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-termi
 A;Reference number: A61512; MUID:81172836; PMID:6163983
 A;Accession: C61512
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-8 <HOL>
 A;Cross-references: UNIPROT:Q7M3S3
 C;Keywords: glycoprotein

Query Match 24.3%; Score 18; DB 2; Length 8;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 DNRSC 12
 | | | |
 Db 2 ENNAC 6

RESULT 15

I57018
 gene Cftr protein - mouse (fragment)
 C;Species: Mus sp. (mouse)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C;Accession: I57018
 R;Dorin, J.R.; Stevenson, B.J.; Fleming, S.; Alton, E.W.; Dickinson, P.; Porteous, D.J.
 Mamm. Genome 5, 465-472, 1994
 A;Title: Long-term survival of the exon 10 insertion cystic fibrosis mutant mouse is a
 A;Reference number: I57018; MUID:95037043; PMID:7949729
 A;Accession: I57018
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-8 <RES>
 A;Cross-references: UNIPROT:Q7M056; GB:S74246; NID:g710482
 C;Genetics:
 A;Gene: Cftr

Query Match 24.3%; Score 18; DB 2; Length 8;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DNRSC 12
 | | | |
 Db 3 DSPSC 7

Search completed: August 3, 2005, 12:40:39
 Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 12:21:19 ; Search time 165 Seconds
(without alignments)
37.242 Million cell updates/sec

Title: US-09-910-582B-10
Perfect score: 74
Sequence: 1 CRSWNKADNRSC 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 4233

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	29.7	12	2	Q93WB7 lupinus lut
2	21	28.4	9	2	O71066 canine dist
3	21	28.4	10	2	Q6LDE2 Qeldez homo sapien
4	21	28.4	11	2	Q6DW13 Qedw13 bos taurus
5	21	28.4	12	2	Q93WF2 Q93wf2 lupinus lut
6	21	28.4	12	2	Q9QVF2 Q9qvf2 rattus sp.
7	20	27.0	11	1	RR2_CONAM P42341 conopholis
8	20	27.0	11	2	Q9T019 Q9t019 brassica ol
9	20	27.0	12	2	Q86CU1 Q86cul drosophila
10	20	27.0	12	2	Q86FU4 Q86fu4 drosophila
11	20	27.0	12	2	Q9ZAM7 Q9zam7 cellvibrio
12	19	25.7	8	2	Q70Y84 Q70y84 plectranthu
13	19	25.7	8	2	Q7M124 Q7m124 kluyvera ci
14	19	25.7	10	2	Q6LBT3 Q6lbt3 mus musculus
15	19	25.7	11	2	Q77908 Q77908 oreochromis
16	19	25.7	12	2	Q9BP48 Q9bp48 conus penna
17	19	25.7	12	2	Q7M272 Q7m272 triticum sp
18	19	25.7	12	2	Q6LEA4 Q6lea4 plasmid rk2
19	18	24.3	8	2	Q7M353 Q7m353 trypanosoma
20	18	24.3	8	2	Q7M056 Q7m056 mus sp. gen
21	18	24.3	8	2	Q9DSN4 Q9dsn4 beet soil-b
22	18	24.3	8	2	Q9DSN5 Q9dsn5 beet soil-b
23	18	24.3	8	2	Q9EP88 Q9ep88 beet soil-b
24	18	24.3	8	2	Q9EP89 Q9ep89 beet soil-b
25	18	24.3	8	2	Q9EP90 Q9ep90 beet soil-b
26	18	24.3	8	2	Q9EQ41 Q9eq41 beet soil-b
27	18	24.3	8	2	Q9EQ04 Q9eq04 beet soil-b
28	18	24.3	8	2	Q9EQ05 Q9eq05 beet soil-b
29	18	24.3	8	2	Q9EQ06 Q9eq06 beet soil-b
30	18	24.3	8	2	Q9EQ07 Q9eq07 beet soil-b
31	18	24.3	9	1	NEF_HV128 P12481 human immun

ALIGNMENTS

32	18	24.3	9	2	Q7KYP6	Q7ky66 homo sapien
33	18	24.3	9	2	Q9UCQ9	Q9ucq9 homo sapien
34	18	24.3	9	2	Q6XBN2	Q6xbn2 vittia pach
35	18	24.3	9	2	Q85G96	Q85g96 pyrrhobyum
36	18	24.3	9	2	Q6VCX0	Q6vcx0 streptomyce
37	18	24.3	9	2	Q9RE35	Q9re35 chlamydia t
38	18	24.3	10	1	SP34_DICMU	F81545 dictyosteli
39	18	24.3	10	2	Q71GZ2	Q71gz2 andrena lim
40	18	24.3	10	2	Q8SAC2	Q8sac2 amblystegiu
41	18	24.3	10	2	Q847B5	Q847b5 bacillus am
42	18	24.3	11	1	LADD_ONCMY	F81018 oncorhynchu
43	18	24.3	11	2	Q35374	Q35374 paramecium
44	18	24.3	11	2	Q6W928	Q6w928 candidatus
45	18	24.3	12	1	RS19_TOBBP	O56251 tomato big
46	18	24.3	12	2	Q96PK0	Q96pk0 homo sapien
47	18	24.3	12	2	Q9H1Z6	Q9h1z6 homo sapien
48	18	24.3	12	2	Q41611	Q41611 human immun
49	17	23.0	8	2	Q71VP0	Q71vp0 ovis aries
50	17	23.0	8	2	O85406	O85406 coxiella bu
51	17	23.0	8	2	O6LAA8	O6laa8 shigella fl
52	17	23.0	8	2	Q7M0L0	Q7m0l0 clostridium
53	17	23.0	8	2	Q98TU5	Q98tu5 xenopus lae
54	17	23.0	8	2	Q7LZ27	Q7l227 raja oxiata
55	17	23.0	10	1	AKHX_LOCMI	P81626 locusta mig
56	17	23.0	10	1	NO40_TOBAC	P55962 nicotiana t
57	17	23.0	10	2	Q7M2Z8	Q7m2z8 bos taurus
58	17	23.0	10	2	Q9TR47	Q9tr47 bos taurus
59	17	23.0	10	2	Q70Y78	Q70y78 plectranthu
60	17	23.0	10	2	Q947R7	Q947r7 solanum tub
61	17	23.0	10	2	Q6TS30	Q6ts30 lycopersico
62	17	23.0	10	2	Q8JFE7	Q8jfe7 ficedula al
63	17	23.0	10	2	Q8J3J3	Q8j3j3 ficedula hy
64	17	23.0	10	2	Q9PRU9	Q9pru9 sparus aura
65	17	23.0	11	1	MLG_THETS	F41989 theromyzon
66	17	23.0	11	2	O60761	O60761 homo sapien
67	17	23.0	12	1	NO40_LOTJA	O22436 lotus japon
68	17	23.0	12	1	NO40_SESRO	O24369 sesbania ro
69	17	23.0	12	2	P92454	P92454 cycas revol
70	17	23.0	12	2	Q37071	Q37071 petunia hyb
71	17	23.0	12	2	Q8LLC3	Q8llc3 trifolium r
72	17	23.0	12	2	Q75729	Q75729 human immun
73	16	21.6	4	1	QCP3_OCTMI	P58649 octopus min
74	16	21.6	8	2	Q64971	Q64971 alfalfa mos
75	16	21.6	8	2	Q6ZZ00	Q6zz00 silene rotu
76	16	21.6	9	2	Q6LAQ1	Q6lad1 rattus norv
77	16	21.6	9	2	O12096	O12096 caprine art
78	16	21.6	9	2	O12098	O12098 caprine art
79	16	21.6	9	2	O12100	O12100 caprine art
80	16	21.6	9	2	O12102	O12102 caprine art
81	16	21.6	9	2	O12104	O12104 caprine art
82	16	21.6	10	1	MP2_MICOC	F81533 microplitis
83	16	21.6	10	2	Q15342	Q15342 homo sapien
84	16	21.6	10	2	Q6M69	Q6m69 potato viru
85	16	21.6	10	2	Q8UT83	Q8ut83 human immun
86	16	21.6	11	1	CEP1_ACHFU	P22790 achatina fu
87	16	21.6	11	1	COR2_PERAM	F11436 periplaneta
88	16	21.6	11	1	Q77914	Q77914 oreochromis
89	16	21.6	11	2	O78118	O78118 oreochromis
90	16	21.6	11	2	O78120	O78120 oreochromis
91	16	21.6	11	2	Q6LD68	Q6ld68 mus sp. acu
92	16	21.6	11	2	Q8CGW6	Q8cgw6 rattus norv
93	16	21.6	12	2	O9BZ49	O9bz49 homo sapien
94	16	21.6	12	2	O77889	O77889 oreochromis
95	16	21.6	12	2	O77890	O77890 oreochromis
96	16	21.6	12	2	O77891	O77891 oreochromis
97	16	21.6	12	2	O77920	O77920 pseudotroph
98	16	21.6	12	2	O12074	O12074 caprine art
99	16	21.6	12	2	O12076	O12076 caprine art
100	16	21.6	12	2	O12078	O12078 caprine art

```

RESULT 1
Q93WB7 ID Q93WB7 PRELIMINARY; PRT; 12 AA.
AC Q93WB7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early nodulin.
GN Name=ENOD40C;
OS Lupinus luteus (Yellow lupine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
OX NCBI_TaxID=3873;
RN [1]
RP SEQUENCE FROM N.A.
RA Podkowinski J., Grabowska B., Kisiel A., Dlugaszewska B.,
RA Nimmagadda G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Podkowinski J., Kisiel A., Grabowska B., Dlugaszewska B.,
RA Nimmagadda G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF352374; AAK51421.1; -.
DR EMBL; AF352373; AAK51420.1; -.
SQ SEQUENCE 12 AA; 1439 MW; 383850887CB326C3 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 5.9e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WNKADNRS 11
| | | |
DB 5 WQKSINGS 12

RESULT 2
O71066 ID O71066 PRELIMINARY; PRT; 9 AA.
AC O71066;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fusion protein (fragment).
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RA Liermann H., Harder T., Haas L.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026234; AAC09164.1; -.
FT NON TER 9
SQ SEQUENCE 9 AA; 1124 MW; F29D045760440441 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 NKADNRS 11
| | | |
DB 3 NRIPNRS 9

RESULT 3
Q6LDE2 ID Q6LDE2 PRELIMINARY; PRT; 10 AA.
AC Q6LDE2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Proacrosin protein (Fragment).
GN Name=proacrosin;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92331659; PubMed=1628652;
RA Vazquez-Levin M.H., Reventos J., Gordon J.W.;
RT "Molecular cloning, sequencing and restriction mapping of the genomic
RT sequence encoding human proacrosin.";
RL Eur. J. Biochem. 207:23-26(1992).
DR EMBL; S40014; AAD13819.1; -.
FT NON TER 10
SQ SEQUENCE 10 AA; 1007 MW; C26972D44AA33DC2 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 7.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DNRSC 12
| | | |
DB 6 DNATC 10

RESULT 4
Q6DW13 ID Q6DW13 PRELIMINARY; PRT; 11 AA.
AC Q6DW13;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Cathepsin B (Fragment).
GN Name=CTSB;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Juszcuk-Kubiak E., Rosochaeki S., Szreder T., Wicinska K.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY639598; AAT58218.1; -.
FT NON TER 11
FT NON TER 11
SQ SEQUENCE 11 AA; 1265 MW; 39C909F87AB1A453 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SWN 5
| | | |
DB 3 SWN 5

RESULT 5
Q93WF2 ID Q93WF2 PRELIMINARY; PRT; 12 AA.
AC Q93WF2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early nodulin.
GN Name=ENOD40B;
OS Lupinus luteus (Yellow lupine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
OX NCBI_TaxID=3873;

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RN [1]
RP SEQUENCE FROM N.A.
RA Podkowinski J., Grabowska B., Kisiel A., Dlugaszewska B.,
RL Nimmagadda G.;
RN Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Kisiel A., Grabowska B., Dlugaszewska B., Nimmagadda G.,
RL Podkowinski J.;
RN Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF352375; AAK51422.1; -
DR EMBL; AF352372; AAK51419.1; -
SQ SEQUENCE 12 AA; 1403 MW; 283958AE7CB326C3 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SWNKA 7
Db 4 SWQKS 8

RESULT 6
Q9QVF2 ID Q9QVF2 PRELIMINARY; PRT; 12 AA.
AC Q9QVF2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TRANSFERRIN-PEPTIDE 21 (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
[1]
RP SEQUENCE.
RX MEDLINE=92165927; PubMed=1791188;
RA Cavanaugh P.G., Nicolson G.L.;
RT "Lung-derived growth factor that stimulates the growth of lung-
RT metastasizing tumor cells: identification as transferrin.";
RL J. Cell. Biochem. 47:261-271(1991).
FT NON TER 1
FT NON TER 12
FT NON TER 12
SQ SEQUENCE 12 AA; 1436 MW; 40AD1DFA420AADD3 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NKAD 8
Db 4 NKAD 7

RESULT 7
RR2_CONAM ID RR2_CONAM STANDARD; PRT; 11 AA.
AC P42341;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Plastid 30S ribosomal protein S2 (Fragment).
GN Name=rrs2;
OS Conopholis americana (Squawroot).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Orobanchaceae; Orobanchaceae; Conopholis.
OX NCBI_TaxID=41179;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92145776; PubMed=1723664;

Taylor G., Wolfe K.H., Morden C.W., Depamphilis C.W., Palmer J.D.;
RT "Lack of a functional plastid trnA(Cys) gene is associated with loss
of photosynthesis in a lineage of parasitic plants.";
Curr. Genet. 20:515-518(1991).
CC -1- SUBCELLULAR LOCATION: Plastid.
CC -1- SIMILARITY: Belongs to the ribosomal protein S2P family.
-----
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CC HAMAP; MF_00291; -.
CC InterPro; IPR001865; Ribosomal_S2.
CC PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
CC PROSITE; PS00963; RIBOSOMAL_S2_2; PARTIAL.
KW Chloroplast; Ribosomal protein.
FT NON TER 11
FT NON TER 11
SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;

Query Match 27.0%; Score 20; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RSWN 5
Db 4 RYWN 7

RESULT 8
Q9TOL9 ID Q9TOL9 PRELIMINARY; PRT; 11 AA.
AC Q9TOL9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SLG5 protein (Fragment).
GN Name=SLG5;
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99264316; PubMed=10330480;
RA Cabrilla D., Delorme V., Garin J., Ruffio-Chable V., Giranton J.L.,
RA Dumas C., Gaudet T., Cock J.M.;
RT "The S15 self-incompatibility haplotype in Brassica includes three S
RT gene family members which are expressed in stigmas.";
RL Plant Cell 11:971-986(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Cock M.J.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18256; CAB41875.1; -.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 11 AA; 1035 MW; CD3806DDA8772AAD CRC64;

Query Match 27.0%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 NKADNRSC 12
Db 2 NAADLGTC 9

```

RESULT 9

Q86CUI ID Q86CUI PRELIMINARY; PRT; 12 AA.
 AC Q86CUI;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Trypsin 1 (Fragment)
 GN Name=Try1; Synonyms=try1;
 OS Drosophila novamexicana.
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=47314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=15010-1031.0;
 RC MEDLINE=22480340; PubMed=12574518; DOI=10.1073/pnas.0336368100;
 RA Wittkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.;
 RT "Drosophila pigmentation evolution: divergent genotypes underlying
 convergent phenotypes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813 (2003).
 DR EMBL; AY165534; AAP21578.1; -;
 DR FlyBase; FBgn0066204; Dnov\Try1.
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1301 MW; DF5820B9A84452D2 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RSW 4
 DB 2 RSW 4

RESULT 10

Q86FU4 ID Q86FU4 PRELIMINARY; PRT; 12 AA.
 AC Q86FU4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Trypsin 1 (Fragment)
 GN Name=Try1; Synonyms=try1;
 OS Drosophila americana (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=40366;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=15010-0951.0;
 RC MEDLINE=22480340; PubMed=12574518; DOI=10.1073/pnas.0336368100;
 RA Wittkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.;
 RT "Drosophila pigmentation evolution: divergent genotypes underlying
 convergent phenotypes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813 (2003).
 DR EMBL; AY165534; AAP21578.1; -;
 DR FlyBase; FBgn0066268; Dame\Try1.
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1301 MW; DF5820B9A84452D2 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RSW 4
 DB 2 RSW 4

RESULT 11

QY 2 RSW 4
 DB 2 RSW 4

Q9ZAM7

AC Q9ZAM7 PRELIMINARY; PRT; 12 AA.
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Endoglucanase (Fragment).
 OS Cellvibrio japonicus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Cellvibrion.
 OX NCBI_TaxID=155077;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cellulosa;
 RX MEDLINE=90014181; PubMed=2507868;
 RA Hall J., Hazlewood G.P., Huskisson N.S., Durrant A.J., Gilbert H.J.;
 RT "Conserved serine-rich sequences in xylanase and cellulase from
 Pseudomonas fluorescens subspecies cellulosa: internal sequence and
 unusual protein processing.";
 RL Mol. Microbiol. 31:1211-1219 (1989).
 DR EMBL; X15429; CAA33470.1; -;
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1419 MW; 590020CF5AB69EB3 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 NRSC 12
 DB 3 NRKC 6

RESULT 12

Q70Y84 ID Q70Y84 PRELIMINARY; PRT; 8 AA.
 AC Q70Y84;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Ribosomal protein (Fragment).
 GN Name=rp16;
 OS Plectranthus buchananii.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Plectranthus.
 OX NCBI_TaxID=204181;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
 RA Paton A., Springate D.A., Sudde S., Otiemo D., Grayer R., Harley M.M.,
 RA Willis F., Simmonds M.S.J., Powell M.P., Savolainen V.;
 RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
 based on three plastid DNA regions.";
 RL Mol. Phylogenet. Evol. 31:277-299 (2004).
 DR EMBL; AJ505379; CAD45500.1; -;
 DR GO; GO:0003735; F:Structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 945 MW; 6EA415A5B5AB5863 CRC64;

Query Match 25.7%; Score 19; DB 2; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.6e+06;
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 WNKADNR 11
 DB 1 WGYCSSRS 8

RESULT 13

QY 4 WNKADNR 11
 DB 1 WGYCSSRS 8

Q7M124
ID Q7M124 PRELIMINARY; PRT; 8 AA.
AC Q7M124;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acylase.
OS Kluyvera citrophila (Kluyvera cryocrescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Kluyvera.
OX NCBI_TaxID=580;
RN [1]
RP SEQUENCE.
RA Martin J., Slade A., Aitken A., Arche R., Virden R.;
RT "Chemical modification of serine at the active site of penicillin
acylase from Kluyvera citrophila.";
RL Biochem. J. 280:659-662(1991).
DR PIR; S19288; S19288.
SQ SEQUENCE 8 AA; 950 MW; CC387042D376944E CRC64;

Query Match 25.7%; Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRSW 4
Db 1 CNMW 4

RESULT 14

Q6LBT3
ID Q6LBT3 PRELIMINARY; PRT; 10 AA.
AC Q6LBT3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ncam gene exon (pi) for neural cell adhesion molecule (NCAM).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RX MEDLINE=89251563; PubMed=2721486;
RA Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille W.;
RT "Differential exon usage involving an unusual splicing mechanism
generates at least eight types of NCAM cDNA in mouse brain.";
RL EMBO J. 8:385-392(1989).
DR EMBL; X14527; CAA32669.1;
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
SQ SEQUENCE 10 AA; 1231 MW; 3689D63B077411B3 CRC64;

Query Match 25.7%; Score 19; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SWNKADR 10
Db 2 SWTRPEK 9

RESULT 15

Q77908
ID Q77908 PRELIMINARY; PRT; 11 AA.
AC Q77908;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 2 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
class II B loci.";
RT Genetics 149:1527-1537(1998).
RL EMBL; AF050019; AAC41358.1; -.
DR EMBL; AF050019; AAC41358.1; -.
FT NON TER 1 1
SQ SEQUENCE 11 AA; 1261 MW; 4346CE9A7EB69EB3 CRC64;

Query Match 25.7%; Score 19; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRSW 5
Db 5 CMCWS 9

Search completed: August 3, 2005, 12:38:36
Job time : 168 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 12:20:34 ; Search time 158 Seconds
(without alignments)
29.374 Million cell updates/sec

Title: US-09-910-582B-10

Perfect score: 74

Sequence: 1 CRSWNKADNRSC 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 520583

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	12	4	AAB30899 Peptide w
2	74	100.0	12	4	AAB59304 Heart hom
3	34	45.9	11	6	ABU59547 RGD bindi
4	33	44.6	12	2	AAR75854 Factor XI
5	32	43.2	11	6	ABU59550 RGD bindi
6	32	43.2	12	2	AAU48838 Membrane
7	32	43.2	12	8	ADF78100 Factor VI
8	31	41.9	11	2	AAR34250 Mutant HT
9	31	41.9	12	2	AAU48661 Membrane
10	31	41.9	12	8	ADF78103 Factor VI
11	30	40.5	10	2	AAR15780 Farnesyl-
12	30	40.5	10	2	AAR49741 Farnesylt
13	30	40.5	10	2	AAR77803 Farnesyl
14	30	40.5	10	2	AAW04433 Farnesyl
15	30	40.5	10	4	AAG96025 Human com
16	30	40.5	11	3	AAB10371 Geranylge
17	30	40.5	11	5	ABB98443 Lamine B
18	30	40.5	11	5	AAO22589 Carboxy t
19	30	40.5	11	5	ABB98445 Lamine B
20	30	40.5	11	5	ABB98447 Lamine B
21	30	40.5	12	8	ADF78096 Factor VI
22	29.5	39.9	11	5	ABP47645 N. mening
23	29.5	39.9	12	5	ABG60538 Selective
24	29	39.2	5	8	ADP06126 Cell adhe
25	29	39.2	6	8	ADP06145 Cell adhe

26	29	39.2	6	8	ADP06127	Cell adhe
27	29	39.2	7	8	ADP06128	Cell adhe
28	29	39.2	7	8	ADP06146	Cell adhe
29	29	39.2	8	8	ADP06129	Cell adhe
30	29	39.2	8	8	ADP06147	Cell adhe
31	29	39.2	8	8	ADP06148	Cell adhe
32	29	39.2	9	8	ADP06130	Cell adhe
33	29	39.2	10	4	AAG83522	Arabidops
34	29	39.2	10	8	ADP06131	Cell adhe
35	29	39.2	10	8	ADP06149	Cell adhe
36	29	39.2	11	6	ABU59549	RGD bindi
37	29	39.2	11	8	ADP06132	Cell adhe
38	29	39.2	11	8	ADP06130	Cell adhe
39	29	39.2	12	3	AAU54523	Human CD4
40	29	39.2	12	7	ADL17593	Human MAG
41	29	39.2	12	8	ADK65054	PP1C-inte
42	29	39.2	12	8	ADP06151	Cell adhe
43	29	39.2	12	8	ADP06133	Cell adhe
44	28	37.8	9	2	AAU10394	T cell ep
45	28	37.8	9	5	ABG80076	MHC class
46	28	37.8	9	8	ADK69015	Epitope l
47	28	37.8	9	8	ADQ10813	Murine he
48	28	37.8	11	6	ABU59552	RGD bindi
49	28	37.8	12	2	AAU48882	Membrane
50	27.5	37.2	9	5	ABP53959	VEGFR-3 b
51	27.5	37.2	9	5	ABJ04511	HUVEC cel
52	27	36.5	8	3	AAU20992	Oligo-cyl
53	27	36.5	9	3	AAU94203	Human cyt
54	27	36.5	9	3	AAU98763	WT1 deriv
55	27	36.5	9	3	AAU98534	WT1 deriv
56	27	36.5	9	3	AAU98652	WT1 deriv
57	27	36.5	9	3	AAU98616	WT1 deriv
58	27	36.5	9	3	AAU98743	WT1 deriv
59	27	36.5	9	3	AAU80202	Human WT1
60	27	36.5	9	4	AAU61948	Human WT1
61	27	36.5	9	4	AAU61984	Human WT1
62	27	36.5	9	4	AAU62095	Mouse WT1
63	27	36.5	9	4	AAU61866	Human WT1
64	27	36.5	9	4	AAU62075	Mouse WT1
65	27	36.5	9	4	AAU68862	Mouse WT1
66	27	36.5	9	4	AAU68633	Human WT1
67	27	36.5	9	4	AAU68715	Human WT1
68	27	36.5	9	4	AAU68751	Human WT1
69	27	36.5	9	4	AAU68842	Mouse WT1
70	27	36.5	9	5	ABU05262	Vascular
71	27	36.5	9	5	ABG33103	Human WT1
72	27	36.5	9	5	ABG33312	Mouse WT1
73	27	36.5	9	5	ABG33332	Mouse WT1
74	27	36.5	9	5	ABG33185	Human WT1
75	27	36.5	9	5	ABG33221	Human WT1
76	27	36.5	9	5	ABG99881	Mouse WT1
77	27	36.5	9	6	ABR44359	Peptide #
78	27	36.5	9	6	ABR38975	Tumour su
79	27	36.5	9	6	ABR44450	WT1 origi
80	27	36.5	9	7	ADB67460	Mouse WT1
81	27	36.5	9	7	ADB67369	Human WT1
82	27	36.5	9	7	ADB67480	Mouse WT1
83	27	36.5	9	7	ADB67251	Human WT1
84	27	36.5	9	7	ADB67333	Human WT1
85	27	36.5	9	7	ADE77829	Synthetic
86	27	36.5	9	7	ADJ80484	Wilm's tu
87	27	36.5	9	7	ADJ80566	Wilm's tu
88	27	36.5	9	7	ADJ80602	Wilm's tu
89	27	36.5	9	7	ADJ80693	Wilm's tu
90	27	36.5	9	8	ADJ80713	Wilm's tu
91	27	36.5	9	8	ADI00714	Human cox
92	27	36.5	9	8	ADJ83613	Murine WT
93	27	36.5	9	8	ADJ83522	Human WT1
94	27	36.5	9	8	ADJ83633	Murine WT
95	27	36.5	9	8	ADJ83404	Human WT1
96	27	36.5	9	8	ADJ83486	Human WT1
97	27	36.5	9	8	ADL57292	Human WT-
98	27	36.5	9	8	ADL57410	Human WT-

99 27 36.5 9 8 ADL57374 AdL57374 Human WT-
100 27 36.5 9 8 ADL57521 AdL57521 Mouse WT-

ALIGNMENTS

RESULT 1
AAB30899
ID AAB30899 standard; peptide; 12 AA.

AC AAB30899;
XX
XX 02-APR-2001 (first entry)
XX
XX Peptide which selectively binds to normal cardiac endothelium.
XX
XX Cardiac endothelium; angiogenic factor; vascular endothelium;
KW peripheral vascular disease; cardiovascular disease; angiogenesis;
KW cardiac neovascularisation.
XX

OS Unidentified.
XX
XX WO200075329-A1.
PN
XX 14-DEC-2000.

XX
XX 31-MAY-2000; 2000WO-US014988.
XX
XX 07-JUN-1999; 99US-00327045.

XX
XX (EDWA-) EDWARDS LIFESCIENCES CORP.
PA
XX (BAXT) BAXTER AG.

XX
XX Levine AJ, Mitterer A, Falkner F, Scheiflinger F, Dorner F;
XX
XX WPI; 2001-091212/10.

XX New chimeric molecules having an angiogenic factor linked to a targeting
PT molecule that binds to a vascular endothelium, useful for increasing
PT cardiac neovascularization, or treating peripheral vascular and
PT cardiovascular diseases.
XX

PS Disclosure; Page 27; 67pp; English.

XX
XX AAB30895-99 represent targeting molecules, which are used to produce the
CC chimeric molecules of the invention. AAB30895-98 selectively bind to
CC normal cardiac endothelium. The specification describes a chimeric
CC molecule comprising an angiogenic factor linked to a targeting molecule
CC that specifically binds to a vascular endothelium. The chimeric molecules
CC are useful for treatment of peripheral vascular or cardiovascular
CC diseases. Specifically, they are useful for inducing or inhibiting
CC angiogenesis, for increasing cardiac neovascularisation in ischemic
CC tissue in the peripheral vascular system
XX

SQ Sequence 12 AA;

Query Match 100.0%; Score 74; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12
Db 1 CRSWNKADNRSC 12
|||||

RESULT 2
AAB59304
ID AAB59304 standard; peptide; 12 AA.

XX
XX AAB59304;
AC
XX 21-MAR-2001 (first entry)
XX

XX Heart homing peptide SEQ ID NO: 10.
DE
XX
KW Heart homing peptide; cardiovascular disease; ischaemic disease;
KW gene therapy.
XX
OS Synthetic.

XX Key Location/Qualifiers
FH Disulfide-bond 1..12
FT /note= "disulfide bond cyclises the peptide"
XX

XX WO200075174-A1.

XX 14-DEC-2000.

XX 31-MAY-2000; 2000WO-US015088.

XX 07-JUN-1999; 99US-00326718.

XX (BURN-) BURNHAM INST.

XX Ruoslahti E, Mackenna DA;
PI
XX WPI; 2001-071059/08.

XX Novel heart homing peptide that selectively homes to normal ischemic and
XX cardiac tissue useful for targeting ischemic tissues for treating
XX ischemic and cardiovascular diseases such as atherosclerosis and
XX restenosis.

XX Claim 2; Page 55; 70pp; English.

XX The present invention provides a number of heart homing peptides which
XX selectively home to cardiac tissue. These can be used in the treatment of
XX cardiovascular and ischaemic diseases, such as atherosclerosis, myocardial
XX thrombosis, restenosis, vasculitis, atherosclerotic aneurysms, myocardial
XX hypertrophy, congenital heart diseases, ischaemic heart disease and
XX anginas, acquired valvular/endocardial diseases, primary myocardial
XX diseases, cardiac tumours and arrhythmias
XX

SQ Sequence 12 AA;

Query Match 100.0%; Score 74; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRSWNKADNRSC 12
Db 1 CRSWNKADNRSC 12
|||||

RESULT 3

ABU59547
ID ABU59547 standard; peptide; 11 AA.

XX
XX ABU59547;
AC

XX 22-APR-2003 (first entry)

XX RGD binding peptide #3.

XX Targeting ligand; bioactive agent; polymer matrix; cancer; cytostatic;
KW cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;
KW fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;
KW tumour; cationic cancer-targeting peptide.

XX Synthetic.
OS

XX US2002041898-A1.

XX 11-APR-2002.

PF 25-JUL-2001; 2001US-00912609.
 XX
 PR 05-JAN-2000; 2000US-00478124.
 PR 31-OCT-2000; 2000US-00703474.
 XX
 PA (UNGE//) UNGER E C.
 PA (MATS//) MATSUNAGA T O.
 PA (RAMA//) RAMASWAMI V.
 PA (ROMA//) ROMANOWSKI M J.
 XX
 PI Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;
 XX WPI; 2003-208921/20.
 DR
 XX Targeted delivery system comprising a bioactive agent homogeneously
 XX dispersed in a targeted matrix is especially useful in cancer therapy.
 PT
 XX
 XX Claim 44; Page 38; 46pp; English.
 PS
 XX The invention relates to a composition comprising a bioactive agent
 CC homogeneously dispersed in a targeted matrix (polymer and targeting
 CC ligand). Also included are a targeted matrix for use as a delivery
 CC vehicle comprising a polymer associated with a targeting ligand,
 CC enhancing the bioavailability of an agent comprising administration of the
 CC the composition and treating cancer comprising administration of the
 CC novel composition. The method is useful for targeted delivery of a drug,
 CC especially in cancer therapy. The targeting ligand may be a peptide.
 CC Examples of targeting peptides are disclosed including cathepsin-D
 CC substrate peptides, peptides targeting receptors in the brain and kidney,
 CC peptides recognising fibronectin- and vitronectin-binding integrins,
 CC peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies,
 CC peptides targeting the angiogenic endothelium of solid tumours, tissue
 CC specific peptides (e.g. of lung, skin, pancreas, intestine, uterus,
 CC adrenal gland and retina), and cationic cancer-targeting peptides. The
 CC present sequence is a peptide targeting ligand disclosed in the invention
 XX
 SQ Sequence 11 AA;
 Query Match 45.9%; Score 34; DB 6; Length 11;
 Best Local Similarity 60.0%; Pred. No. 1e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 3 SWNKADNRSC 12
 | : | | | | |
 Db 2 SFGKGDNRIC 11
 RESULT 4
 AAR75854
 ID AAR75854 standard; peptide; 12 AA.
 XX
 AC AAR75854;
 XX
 XX 11-MAR-1996 (first entry)
 DT
 XX
 DE Factor XI(a) platelet binding site peptide analogue.
 XX
 XX Factor XI(a); platelet binding site; peptide analogue; thrombosis;
 KW antithrombotic agent; intrinsic coagulation.
 KW
 XX Synthetic.
 OS
 XX
 PI Key Location/Qualifiers
 FH Disulfide-bond 1. .12
 FT
 XX
 XX WO9517420-A1.
 PN
 XX
 XX 29-JUN-1995.
 PD
 XX
 XX 02-DEC-1994; 94WO-US013885.
 PF
 XX
 XX 22-DEC-1993; 93US-00172002.
 PR
 XX

(UTEM) UNIV TEMPLE.
 (UYJE-) UNIV JEFFERSON THOMAS.
 Walsh PN, Baglia FA, Jameson BA;
 WPI; 1995-240608/31.
 DR
 XX Peptide analogues of the factor XI platelet binding site - used to
 PT specifically inhibit coagulation reactions involving factor XI and factor
 PT XIa, for improved treatment of thrombosis.
 PT
 XX Claim 10; Page 79; 99pp; English.
 PS
 XX AAR75854 is a factor XI(a) platelet binding site peptide analogue, useful
 CC as an antithrombotic agent. The peptide specifically inhibits intrinsic
 CC coagulation reactions, while leaving extrinsic reactions intact. This
 CC permits normal hemostatic plug formation at a site of vascular injury,
 CC minimising the risk of bleeding during antithrombotic therapy
 XX
 SQ Sequence 12 AA;
 Query Match 44.6%; Score 33; DB 2; Length 12;
 Best Local Similarity 41.7%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CRSWNKADNRSC 12
 | : | | | | |
 Db 1 CPWPKEQRPC 12
 RESULT 5
 ABUS9550
 ID ABUS9550 standard; peptide; 11 AA.
 XX
 AC ABUS9550;
 XX
 XX 22-APR-2003 (first entry)
 DT
 XX
 DE RGD binding peptide #6.
 XX
 KW Targeting ligand; bioactive agent; polymer matrix; cancer; cytostatic;
 KW cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;
 KW fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;
 KW tumour; cationic cancer-targeting peptide.
 XX
 OS Synthetic.
 XX
 XX US2002041898-A1.
 PN
 XX
 PD 11-APR-2002.
 XX
 XX 25-JUL-2001; 2001US-00912609.
 PF
 XX
 XX 05-JAN-2000; 2000US-00478124.
 PR
 PR 31-OCT-2000; 2000US-00703474.
 XX
 XX (UNGE//) UNGER E C.
 PA (MATS//) MATSUNAGA T O.
 PA (RAMA//) RAMASWAMI V.
 PA (ROMA//) ROMANOWSKI M J.
 XX
 XX Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;
 PI WPI; 2003-208921/20.
 XX
 XX Targeted delivery system comprising a bioactive agent homogeneously
 PT dispersed in a targeted matrix is especially useful in cancer therapy.
 PT
 XX Claim 44; Page 38; 46pp; English.
 PS
 XX The invention relates to a composition comprising a bioactive agent
 CC homogeneously dispersed in a targeted matrix (polymer and targeting
 CC ligand). Also included are a targeted matrix for use as a delivery
 CC vehicle comprising a polymer associated with a targeting ligand,
 CC enhancing the bioavailability of an agent comprising administration of the
 CC the composition and treating cancer comprising administration of the
 CC novel composition. The method is useful for targeted delivery of a drug,
 CC especially in cancer therapy. The targeting ligand may be a peptide.
 CC Examples of targeting peptides are disclosed including cathepsin-D
 CC substrate peptides, peptides targeting receptors in the brain and kidney,
 CC peptides recognising fibronectin- and vitronectin-binding integrins,
 CC peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies,
 CC peptides targeting the angiogenic endothelium of solid tumours, tissue
 CC specific peptides (e.g. of lung, skin, pancreas, intestine, uterus,
 CC adrenal gland and retina), and cationic cancer-targeting peptides. The
 CC present sequence is a peptide targeting ligand disclosed in the invention
 XX

CC vehicle comprising a polymer associated with a targeting ligand,
 CC enhancing the bioavailability of an agent comprising administration of
 CC the composition and treating cancer comprising administration of the
 CC novel composition. The method is useful for targeted delivery of a drug,
 CC especially in cancer therapy. The targeting ligand may be a peptide.
 CC Examples of targeting peptides are disclosed including cathepsin-D
 CC substrate peptides, peptides targeting receptors in the brain and kidney,
 CC peptides recognising fibronectin- and vitronectin-binding integrins,
 CC peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies,
 CC peptides targeting the angiogenic endothelium of solid tumours, tissue
 CC specific peptides (e.g. of lung, skin, pancreas, intestine, uterus,
 CC adrenal gland and retina), and cationic cancer- targeting peptides. The
 CC present sequence is a peptide targeting ligand disclosed in the invention
 XX

SQ Sequence 11 AA;

Query Match 43.2%; Score 32; DB 6; Length 11;
 Best Local Similarity 50.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 SWNKADNRSC 12
 | : : | | |
 Db 2 SFGRADRRNC 11

RESULT 6
 AAY48838
 ID AAY48838 standard; peptide; 12 AA.

AC AAY48838;
 XX
 XX 20-MAR-2003 (revised)
 DT 10-DEC-1999 (first entry)
 XX
 DE Membrane dipeptidase-binding retina homing peptide #24.
 XX
 XX Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
 KW membrane dipeptidase.

XX Synthetic.
 OS Homo sapiens.
 XX
 XX WO9946284-A2.
 DN
 XX 16-SEP-1999.

XX 10-MAR-1999; 99WO-US005284.
 XX
 XX 13-MAR-1998; 98US-00042107.
 PR
 XX 26-FEB-1999; 99US-00258754.

XX (BURN-) BURNHAM INST.

XX Rajotte D, Pasqualini R, Ruoslahti ET;

XX WPI; 1999-571717/48.

XX New peptides which selectively home to organs or tissues, used for, e.g.
 PT identifying target ligands and for therapy of pathological conditions.

XX Claim 28; Page 149; 193pp; English.

XX The present invention describes peptides that selectively home to a
 CC tissue or organ. The peptides can be used for identifying an organ or
 CC tissue, for identifying a target molecule expressed by an organ or tissue
 CC or for treating an organ or tissue pathology, where the organ or tissue
 CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,
 CC adrenal gland, liver, and lymph node. The peptide bind to the membrane
 CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are
 CC used in the exemplification of the present invention. (Updated on 20-MAR-
 CC 2003 to correct PR field.)
 XX

SQ Sequence 12 AA;

Query Match 43.2%; Score 32; DB 2; Length 12;
 Best Local Similarity 41.7%; Pred. No. 2.4e+02;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CRSWNKADNRSC 12
 | : : | | |
 Db 1 CORVNSVENASC 12

RESULT 7
 ADF78100
 ID ADF78100 standard; peptide; 12 AA.

AC ADF78100;
 XX
 XX 26-FEB-2004 (first entry)
 DT
 XX Factor VIII peptidic mimic SEQ ID NO:13.

DE
 XX peptidic mimic; pseudopeptidic mimic; factor VIII; haemophilia A;
 KW haemostatic; immunosuppressive; autoimmune disorder; haemorrhage.
 XX
 XX Synthetic.
 OS
 XX FR2830865-A1.
 PN
 XX 18-APR-2003.
 PD
 XX 17-OCT-2001; 2001FR-00013360.
 PF
 XX 17-OCT-2001; 2001FR-00013360.
 PR
 XX (CNRS) CNRS CENT NAT RECH SCI.

XX Granier C, Villard S;

XX WPI; 2004-064179/07.

XX Peptide and pseudopeptide mimics of factor VIII that prevent disorders
 PT due to the appearance of antibodies against factor VIII in hemophilic
 PT patients.

XX Claim 10; SEQ ID NO 13; 36pp; French.

XX The invention relates to the novel use of peptidic and pseudopeptidic
 CC mimics of factor VIII. The peptidic and pseudopeptidic mimics of factor
 CC VIII are useful in medicines for the prevention and treatment of
 CC disorders caused by the appearance of antibodies against endogenous or
 CC exogenous factor VIII or its derivatives, which may be recombinant or
 CC not, administered in cases of haemophilia A. A peptide of the invention
 CC has haemostatic, and immunosuppressive activity. The compounds of the
 CC invention are useful in the prevention and treatment of autoimmune
 CC disorders and haemorrhage in patients with haemophilia A, especially
 CC those that develop antibodies against factor VIII. The present sequence
 CC is used in the exemplification of the invention.

SQ Sequence 12 AA;

Query Match 43.2%; Score 32; DB 8; Length 12;
 Best Local Similarity 33.3%; Pred. No. 2.4e+02;
 Matches 4; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRSWNKADNRSC 12
 | : : | | |
 Db 1 CSKWHNRSKRHC 12

RESULT 8
 AAR34250
 ID AAR34250 standard; peptide; 11 AA.
 XX

AC AAR34250;
 XX
 XX 25-MAR-2003 (revised)
 DT 04-AUG-1993 (first entry)
 XX
 DE Mutant HTLV-I residues 88-98, peptide 2L-1.4.
 XX
 KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
 KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.
 XX
 OS Synthetic.
 XX
 PN W09306843-A1.
 XX
 XX 15-APR-1993.
 XX
 XX
 PF 08-OCT-1992; 92WO-US008405.
 XX
 XX 08-OCT-1991; 91US-00771553.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Palker TV, Haynes BF;
 XX
 XX WPI; 1993-134125/16.
 XX
 XX
 PT Antigenic determinant peptide(s) of HTLV envelope glyco.protein - useful
 PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.
 XX
 XX Example 7; Page 32; 50pp; English.
 XX
 CC To determine which amino acids within the HTLV-I envelope amino acids 88-
 CC 98 were required for absorption of neutralising anti-peptide antibodies
 CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
 CC sequential amino acids were each replaced by the amino acid alanine.
 CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
 CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
 CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 41.9%; Score 31; DB 2; Length 11;
 Best Local Similarity 62.5%; Pred. No. 3.1e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 WNKADNRS 11
 DB 1 WTKAPNEN 8
 |||||
 |||||
 RESULT 9
 AAY48661
 ID AAY48661 standard; peptide; 12 AA.
 XX
 AC AAY48661;
 XX
 XX 20-MAR-2003 (revised)
 DT 10-DEC-1999 (first entry)
 XX
 XX Membrane dipeptidase-binding lung homing peptide #32.
 DE
 XX Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
 KW membrane dipeptidase.
 XX
 XX Synthetic.
 OS
 OS Homo sapiens.
 XX
 PN W09946284-A2.
 XX
 XX 16-SEP-1999.
 PD
 XX

PF 10-MAR-1999; 99WO-US005284.
 XX
 XX 13-MAR-1998; 98US-00042107.
 PR 26-FEB-1999; 99US-00258754.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 XX Rajotte D, Pasqualini R, Ruoslahti EI;
 PI WPI; 1999-571717/48.
 DR
 XX
 XX New peptides which selectively home to organs or tissues, used for, e.g.
 PT identifying target ligands and for therapy of pathological conditions.
 PT
 XX Claim 11; Page 144; 193pp; English.
 XX
 XX The present invention describes peptides that selectively home to a
 CC tissue or organ. The peptides can be used for identifying an organ or
 CC tissue, for identifying a target molecule expressed by an organ or tissue
 CC or for treating an organ or tissue pathology, where the organ or tissue
 CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,
 CC adrenal gland, liver and lymph node. The peptide bind to the membrane
 CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are
 CC used in the exemplification of the present invention. (Updated on 20-MAR-
 CC 2003 to correct PR field.)
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 41.9%; Score 31; DB 2; Length 12;
 Best Local Similarity 33.3%; Pred. No. 3.4e+02;
 Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CRSWNKADNRSC 12
 |||||
 |||||
 DB 1 CRPWHNQAHTEC 12
 |||||
 |||||
 RESULT 10
 ADF78103
 ID ADF78103 standard; peptide; 12 AA.
 XX
 AC ADF78103;
 XX
 XX 26-FEB-2004 (first entry)
 DT
 XX Factor VIII peptidic mimic SEQ ID NO:16.
 DE
 XX Peptidic mimic; pseudopeptidic mimic; factor VIII; haemophilia A;
 KW haemostatic; immunosuppressive; autoimmune disorder; haemorrhage..
 KW
 XX Synthetic.
 OS
 XX FR2830865-A1.
 PN
 XX 18-APR-2003.
 PD
 XX 17-OCT-2001; 2001FR-00013360.
 PF
 XX 17-OCT-2001; 2001FR-00013360.
 PR
 XX (CNRS) CNRS CENT NAT RECH SCI.
 PA
 XX Granier C, Villard S;
 PI WPI; 2004-064179/07.
 DR
 XX Peptide and pseudopeptide mimics of factor VIII that prevent disorders
 PT due to the appearance of antibodies against factor VIII in hemophilic
 PT patients.
 PT
 XX Claim 10; SEQ ID NO 16; 36pp; French.
 PS
 XX The invention relates to the novel use of peptidic and pseudopeptidic
 CC

CC mimics of factor VIII. The peptidic and pseudopeptidic mimics of factor
 CC VIII are useful in medicines for the prevention and treatment of
 CC disorders caused by the appearance of antibodies against endogenous or
 CC exogenous factor VIII or its derivatives, which may be recombinant or
 CC not, administered in cases of haemophilia A. A peptide of the invention
 CC has haemostatic, and immunosuppressive activity. The compounds of the
 CC invention are useful in the prevention and treatment of autoimmune
 CC disorders and haemorrhage in patients with haemophilia A, especially
 CC those that develop antibodies against factor VIII. The present sequence
 CC is used in the exemplification of the invention.

XX
 SQ Sequence 12 AA;

Query Match 41.9%; Score 31; DB 8; Length 12;
 Best Local Similarity 33.3%; Pred. No. 3.4e+02;
 Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 CRSWNKADNRSC 12
 | | | | |
 Db 1 CMKWSNRSSRWC 12

RESULT 11
 AAR15780
 ID AAR15780 standard; protein; 10 AA.

XX
 AC AAR15780;

XX
 DT 25-MAR-2003 (revised)
 DT 09-JAN-2003 (revised)
 DT 29-JAN-1992 (first entry)

XX Farnesyl-protein transferase inhibitor (33).

XX Farnesyl; transferase; FT; inhibitor; p21ras; rat.

XX Synthetic.

PH Key Location/Qualifiers
 FT Peptide 7. 10

XX WO9116340-A.

XX 31-OCT-1991.

XX 18-APR-1990; 90US-00510706.

XX 18-APR-1990; 90US-00510706.

XX 20-NOV-1990; 90US-00615715.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Brown MS, Goldstein JL, Reiss Y;

XX WPI; 1991-339750/46.

XX Compn. comprising purified farnesyl-protein transferase - used to
 PT inhibit attachment of farnesyl moiety to RAS protein in malignant cells
 PT and to treat cancer.

XX Claim 25; Page 68; 87pp; English.

XX This peptide, the fragment indicated in the features, or the peptides
 CC represented in AAR15751-81, AAR14723 and AAR14711 inhibit the rat FTS
 CC represented in AAR14712-22. They show FT inhibition at an IC50 of 0.01-10
 CC microm. The most potent inhibitors are ones in which phenylalanine occurs
 CC at the third position of a tetrapeptide whose N-terminus is cysteine. The
 CC inhibitors have a farnesyl acceptor or inhibitor sequence within its
 CC structure and are capable of inhibiting the farnesylation of p21ras by
 CC FT. See also AAR14711-23 and AAR14541-47. (Updated on 09-JAN-2003 to add
 CC missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 10 AA;

Query Match 40.5%; Score 30; DB 2; Length 10;
 Best Local Similarity 71.4%; Pred. No. 4e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 KADNRSC 12
 : | | | | |

Db 1 RASNRSC 7

RESULT 12
 AAR49741
 ID AAR49741 standard; peptide; 10 AA.

XX
 AC AAR49741;

XX
 DT 25-MAR-2003 (revised)
 DT 08-AUG-1994 (first entry)

XX Farnesyltransferase-inhibitor.

XX Farnesyltransferase-inhibitor; farnesyltransferase; FT; p21ras;
 KW ras protein; farnesylation; cancer therapy.

XX Synthetic.

XX WO9404561-A1.

XX 03-MAR-1994.

XX 24-AUG-1993; 93WO-US008062.

XX 24-AUG-1992; 92US-00935087.

XX (TEXA) UNIV TEXAS SYSTEM.

XX (GETH) GENENTECH INC.

XX Brown MS, Goldstein JL, Reiss Y, Marsters JC;

XX WPI; 1994-083105/10.

XX New farnesyl-transferase inhibitors - used for inhibiting attachment of a
 PT farnesyl moiety to a p21ras protein in malignant cells.

XX Disclosure; Page 33; 183pp; English.

XX Peptides given in AAR49741-75, AAR49777-78 and AAR49785-88, which include
 CC a family of tetrapeptides based on the recognition site (AAR49776) of
 CC farnesyltransferase (FT), are potential anticancer agents that inhibit
 CC FT, thereby preventing expression of p21ras. (Updated on 25-MAR-2003 to
 CC correct PN field.)

XX Sequence 10 AA;

Query Match 40.5%; Score 30; DB 2; Length 10;
 Best Local Similarity 71.4%; Pred. No. 4e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 KADNRSC 12
 : | | | | |

Db 1 RASNRSC 7

RESULT 13
 AAR77803
 ID AAR77803 standard; protein; 10 AA.

XX
 AC AAR77803;

XX 25-MAR-2003 (revised)

DT 23-JAN-1996 (first entry)

XX Farnesyl transferase inhibitor peptide, RASNRSCAIM.

XX Farnesyl transferase; inhibitor; cancer; ras; p21.
 XX Synthetic.
 XX US5420245-A.
 XX 30-MAY-1995.
 XX 03-APR-1992; 92US-00863169.
 XX 18-APR-1990; 90US-00510706.
 XX 20-NOV-1990; 90US-00615715.
 XX 16-JAN-1992; 92US-00822011.
 XX (TEXA) UNIV TEXAS.
 XX Reiss Y, Goldstein JL, Brown MS;
 XX WPI; 1995-206308/27.
 XX New farnesyl transferase inhibitor peptide(s) - based on farnesyl
 PT acceptor substrate carboxy terminal sequences, used for the treatment of
 PT cancer.
 XX Claim 2; Col 61; 55pp; English.
 XX AAR77801-R77804 are peptide inhibitors of farnesyl transferase. They all
 CC have a carboxyl terminal sequence obeying the generic formula -C(AAX,
 CC where C= cysteine, A= any aliphatic, aromatic or hydroxy amino acid and
 CC X= any normal amino acid. Farnesyl transferase is involved in the
 CC farnesylation of various cellular proteins including the cancer related
 CC ras proteins. The transforming activity of ras is dependent on the
 CC localisation of the protein to membranes, a property which is thought to
 CC be dependent upon the addition of farnesyl groups. The peptide inhibitors
 CC are useful for treating cancers and ras-related cancers in particular.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX SQ Sequence 10 AA;
 Query Match 40.5%; Score 30; DB 2; Length 10;
 Best Local Similarity 71.4%; Pred. No. 4e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 6 KADNRSC 12
 Db :| |||||
 1 RASNRSC 7
 RESULT 14
 ID AAW04433 standard; peptide; 10 AA.
 AC AAW04433;
 XX 30-JUL-1997 (first entry)
 XX Farnesyl transferase peptide inhibitor used in cancer treatment.
 XX Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl;
 KW ras protein; K-ras B; malignant; detection; identification.
 XX Synthetic.
 OS WO9634113-A2.
 PN 31-OCT-1996.
 XX 29-APR-1996; 96WO-US005969.
 XX 27-APR-1995; 95US-00429964.
 XX (TEXA) UNIV TEXAS SYSTEM.

XX Brown MS, Goldstein JL, James GL;
 XX WPI; 1996-497642/49.
 XX Assay for farnesyl transferase activity - by determining ability to
 PT transfer farnesyl moiety to K-Ras B protein, partic. useful for
 PT identifying inhibitors.
 XX Disclosure; Page 33; 257pp; English.
 XX AAW04433-W04465 are peptide inhibitors of farnesyl transferase (FT)
 CC activity. The peptides block the attachment of prenyl groups to ras
 CC proteins in malignant cells of patients suffering from cancer or a
 CC precancerous state and as such are used to treat cancer. The peptides
 CC were identified by determining the ability of candidate substances to
 CC inhibit a FT enzyme, by inhibiting the transfer of a farnesyl moiety to a
 CC K-RasB protein
 XX SQ Sequence 10 AA;
 Query Match 40.5%; Score 30; DB 2; Length 10;
 Best Local Similarity 71.4%; Pred. No. 4e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 6 KADNRSC 12
 Db :| |||||
 1 RASNRSC 7
 RESULT 15
 ID AAG96025 standard; peptide; 10 AA.
 XX AAG96025;
 XX 18-SEP-2001 (first entry)
 XX Human complementary peptide, SEQ ID NO: 2219.
 XX Human; complementary peptide; ligand; drug discovery; drug design.
 XX Homo sapiens.
 XX WO200142277-A2.
 XX 14-JUN-2001.
 XX 13-DEC-2000; 2000WO-GB004776.
 XX 13-DEC-1999; 99GB-00029464.
 XX (PROT-) PROTEOM LTD.
 XX Roberts GW, Heal JR;
 XX WPI; 2001-408419/43.
 XX A set of peptide ligands consisting of specific complementary peptides to
 PT proteins encoded by genes of the human genome, useful in an assay for
 PT screening and identifying of one or more novel peptides which are drug
 PT candidates or pro-drugs.
 XX Example 4; Page 360; 646pp; English.
 XX The invention relates to a set of complementary peptide ligands generated
 CC from the human genome. The complementary peptides interact with their
 CC relevant target proteins encoded in the human genome. They can be used as
 CC reagents in drug discovery and as lead ligands to facilitate drug design
 CC and development. The present sequence is a complementary peptide provided
 CC in the specification
 XX SQ Sequence 10 AA;

Query Match 40.5%; Score 30; DB 4; Length 10;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRSNKADN 9
| : | | |
Db 1 CQRWEKLQN 9

Search completed: August 3, 2005, 12:35:45
Job time : 161 secs

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OM protein - protein search, using sw model

Run on: August 3, 2005, 12:30:30 ; Search time 41 Seconds
(without alignments)
21.849 Million cell updates/sec

Title: US-09-910-582B-10

Perfect score: 74

Sequence: 1 CRWNKADNRSC 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 135920

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTCUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	12	3	US-09-326-718-10
2	32	43.2	12	3	US-09-258-754-244
3	32	43.2	12	3	US-09-042-107-244
4	32	43.2	12	4	US-09-722-250D-244
5	32	43.2	12	4	US-09-676-475A-244
6	31	41.9	11	1	US-08-116-733-34
7	31	41.9	12	3	US-09-258-754-82
8	31	41.9	12	3	US-09-042-107-82
9	31	41.9	12	4	US-09-722-250D-82
10	31	41.9	12	4	US-09-676-475A-82
11	30	40.5	10	2	US-08-429-964-15
12	30	40.5	10	5	PCT-US93-08062-15
13	29	39.2	12	3	US-09-100-409A-24
14	28	37.8	11	5	PCT-US94-01234-71
15	28	37.8	12	3	US-09-258-754-263
16	28	37.8	12	3	US-09-042-107-263
17	28	37.8	12	4	US-09-722-250D-263
18	28	37.8	12	4	US-09-676-475A-263
19	27	36.5	11	8	US-08-990-015-11
20	27	36.5	11	5	PCT-US94-01234-69
21	26	35.1	6	1	US-08-375-911A-4
22	26	35.1	7	4	US-09-036-461-1
23	26	35.1	11	1	US-08-116-733-1
24	26	35.1	11	1	US-08-116-733-38
25	26	35.1	11	1	US-08-116-733-39
26	26	35.1	11	1	US-08-116-733-40
27	26	35.1	11	1	US-08-116-733-41

28	35.1	12	3	US-09-258-754-232	Sequence 232, App
29	35.1	12	3	US-09-042-107-232	Sequence 232, App
30	35.1	12	4	US-09-722-250D-232	Sequence 232, App
31	35.1	12	4	US-09-676-475A-232	Sequence 232, App
32	34.5	12	3	US-09-258-754-64	Sequence 64, Appl
33	34.5	9	3	US-09-042-107-64	Sequence 64, Appl
34	34.5	9	4	US-09-722-250D-64	Sequence 64, Appl
35	34.5	9	4	US-09-676-475A-64	Sequence 64, Appl
36	33.8	7	1	US-08-460-343B-6	Sequence 6, Appl
37	33.8	7	1	US-08-398-028B-6	Sequence 6, Appl
38	33.8	7	2	US-08-504-265B-6	Sequence 6, Appl
39	33.8	8	5	PCT-US95-11127-15	Sequence 15, Appl
40	33.8	9	3	US-09-258-754-378	Sequence 378, App
41	33.8	9	3	US-09-042-107-378	Sequence 378, App
42	33.8	9	4	US-09-722-250D-378	Sequence 378, App
43	33.8	9	4	US-09-676-475A-378	Sequence 378, App
44	33.8	10	3	US-08-925-002-9	Sequence 9, Appl
45	33.8	10	3	US-08-893-526A-14	Sequence 14, Appl
46	33.8	10	3	US-08-630-915A-46	Sequence 46, Appl
47	33.8	10	4	US-09-910-552-9	Sequence 9, Appl
48	33.8	10	4	US-09-879-957-46	Sequence 46, Appl
49	33.8	11	1	US-08-116-733-35	Sequence 35, Appl
50	33.8	11	5	PCT-US94-01234-12	Sequence 12, Appl
51	33.8	12	1	US-07-778-233B-44	Sequence 44, Appl
52	33.8	12	1	US-07-963-321-44	Sequence 44, Appl
53	33.8	12	1	US-08-290-641-44	Sequence 44, Appl
54	33.8	12	1	US-08-548-540-44	Sequence 44, Appl
55	33.8	12	5	PCT-US96-09809-44	Sequence 44, Appl
56	33.1	10	1	US-08-077-797A-7	Sequence 7, Appl
57	33.1	10	4	US-09-546-013-36	Sequence 36, Appl
58	33.1	10	5	PCT-US94-01238-7	Sequence 7, Appl
59	33.1	11	4	US-09-069-827A-40	Sequence 40, Appl
60	32.4	6	3	US-09-270-957-32	Sequence 32, Appl
61	32.4	5	4	US-09-258-754-173	Sequence 173, App
62	32.4	6	3	US-09-042-107-173	Sequence 173, App
63	32.4	6	4	US-09-722-250D-173	Sequence 173, App
64	32.4	6	4	US-09-676-475A-173	Sequence 173, App
65	32.4	7	1	US-08-253-854-68	Sequence 68, Appl
66	32.4	7	4	US-09-535-852-952	Sequence 952, App
67	32.4	7	4	US-09-535-852-1008	Sequence 1008, App
68	32.4	8	1	US-08-526-710-7	Sequence 7, Appl
69	32.4	8	3	US-08-862-855-7	Sequence 7, Appl
70	32.4	8	3	US-09-226-985-7	Sequence 7, Appl
71	32.4	8	3	US-09-227-906-7	Sequence 7, Appl
72	32.4	8	4	US-09-535-852-959	Sequence 959, App
73	32.4	8	4	US-09-535-852-1015	Sequence 1015, App
74	32.4	8	4	US-09-535-852-1233	Sequence 1233, App
75	32.4	8	4	US-09-535-852-1281	Sequence 1281, App
76	32.4	8	4	US-09-228-866-7	Sequence 7, Appl
77	32.4	9	1	US-08-526-710-13	Sequence 13, Appl
78	32.4	9	3	US-08-862-855-13	Sequence 13, Appl
79	32.4	9	3	US-09-258-754-328	Sequence 328, App
80	32.4	9	3	US-09-042-107-328	Sequence 328, App
81	32.4	9	3	US-09-226-985-13	Sequence 13, Appl
82	32.4	9	3	US-09-227-906-13	Sequence 13, Appl
83	32.4	9	4	US-09-722-250D-328	Sequence 328, App
84	32.4	9	4	US-09-535-852-1038	Sequence 1038, App
85	32.4	9	4	US-09-535-852-1039	Sequence 1039, App
86	32.4	9	4	US-09-535-852-1240	Sequence 1240, App
87	32.4	9	4	US-09-535-852-1288	Sequence 1288, App
88	32.4	9	4	US-09-228-866-13	Sequence 13, Appl
89	32.4	9	4	US-09-676-475A-328	Sequence 328, App
90	32.4	10	4	US-09-535-852-1045	Sequence 1045, App
91	32.4	10	4	US-09-535-852-1046	Sequence 1046, App
92	32.4	11	1	US-08-116-733-32	Sequence 32, Appl
93	32.4	12	2	US-08-764-640-84	Sequence 84, Appl
94	32.4	12	3	US-08-973-225-84	Sequence 84, Appl
95	32.4	12	3	US-09-244-298A-84	Sequence 84, Appl
96	32.4	12	3	US-09-258-754-236	Sequence 236, App
97	32.4	12	3	US-09-042-107-236	Sequence 236, App
98	32.4	12	3	US-09-516-704-84	Sequence 84, Appl
99	32.4	12	3	US-09-025-769B-184	Sequence 184, App
100	32.4	12	4	US-09-549-090-84	Sequence 84, Appl

ALIGNMENTS

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RESULT 1
US-09-326-718-10
US-09-326-718-10, Application US/09326718
Patent No. 6303573
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: MacKenna, Deidre A.
TITLE OF INVENTION: Heart Homing Peptides
TITLE OF INVENTION: Using Same
FILE REFERENCE: P-LJ 3512
CURRENT APPLICATION NUMBER: US/09/326,718
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic construct
US-09-326-718-10

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Query Match      100.0%; Score 74; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CRSWNKADNRSC 12
|||
Db 1 CRSWNKADNRSC 12

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RESULT 2
US-09-258-754-244
; Sequence 244, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; FILE OF INVENTION: Membrane Diptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 244
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-244

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Query Match 43.2%; Score 32; DB 3; Length 12;
Best Local Similarity 41.7%; Pred. No. 82;
Matches 5; Conservative 2; Mismatches 5; Indels 0;
Gaps 0;

Qy	1	CRSWNKADNRSC	12
		: :	
Dp	1	CORVNSVENASC	12

RESULT 3
US-09-042-107-244
; Sequence 244, Application US/09042107

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; Patent No. 6232287
;
; GENERAL INFORMATION:
;
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 244
;
; LENGTH: 12
; TYPE: PRT
;
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-042-107-244

```

Query Match 43.2%; Score 32; DB 3; Length 12;
Best Local Similarity 41.7%; Pred. No. 82;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12
 | : | : ||
Db 1 CORVNSVENASC 12

RESULT 4
US-09-722-250D-244
; Sequence 244, Application US/097222250D

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? GENERAL INFORMATION:
? APPLICANT: Ruoslahti, Erkki
? APPLICANT: Pasqualini, Renata
? TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
? TITLE OF INVENTION: Tissues
? FILE REFERENCE: P-LJ 4514
? CURRENT APPLICATION NUMBER: US/09/722,250D
? CURRENT FILING DATE: 2000-11-22
? PRIOR APPLICATION NUMBER: US 09/042,107
? PRIOR FILING DATE: 1998-03-13
? NUMBER OF SEQ ID NOS: 437
? SOFTWARE: Patentin Ver. 2.0
? SEQ ID NO 244
? LENGTH: 12
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-244

```

Query Match 43.2%; Score 32; DB 4; Length 12;
Best Local Similarity 41.7%; Pred. No. 82;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy	1	CRS	W	N	K	A	D	N	R	S	12
		:	:	:	:	:	:	:	:	:	
pb	1	COR	V	N	S	V	E	N	A	S	12

RESULT 5
US-09-676-475A-244
; Sequence 244, Application US/09676475A

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:
: GENERAL INFORMATION:
:
: APPLICANT: Ruoslahti, Erkki
:
: APPLICANT: Pasqualini, Renata
:
: APPLICANT: Rajotte, Daniel
:
: TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
:
: TITLE OF INVENTION: Membrane Dipeptidase
:
: FILE REFERENCE: P-LA 4377
:
: CURRENT APPLICATION NUMBER: US/09/676,475A
:
:

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; CURRENT FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 244
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-676-475A-244

Query Match 43.2%; Score 32; DB 4; Length 12;
Best Local Similarity 41.7%; Pred. No. 82;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12
Db 1 CORVNSVENASC 12

RESULT 6
US-08-116-733-34
; Sequence 34, Application US/08116733
; Patent No. 5516632
; GENERAL INFORMATION:
; APPLICANT: PALKER, Thomas J.
; APPLICANT: HAYNES, Barton F.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,733
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-733-34

Query Match 41.9%; Score 31; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WNKADNES 11
Db 1 WTKAPNRN 8

RESULT 7

US-09-258-754-82
; Sequence 82, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-82

Query Match 41.9%; Score 31; DB 3; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12
Db 1 CRPWHNQAHTEC 12

RESULT 8
US-09-042-107-82
; Sequence 82, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-82

Query Match 41.9%; Score 31; DB 3; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12
Db 1 CRPWHNQAHTEC 12

RESULT 9
US-09-722-250D-82
; Sequence 82, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues

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; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-82

Query Match 41.9%; Score 31; DB 4; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12
Db 1 CRPHNQAHTEC 12

RESULT 10
US-09-676-475A-82
; Sequence 82, Application US/09676475A
; Patent No. 6784153
; GENERAL INFORMATION:
; APPLICANT: Ruolahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LA 4377
; CURRENT APPLICATION NUMBER: US/09/676,475A
; CURRENT FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-676-475A-82

Query Match 41.9%; Score 31; DB 4; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12
Db 1 CRPHNQAHTEC 12

RESULT 11
US-08-429-964-15
; Sequence 15, Application US/08429964
; Patent No. 5962243
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: REISS, YUVAL
; APPLICANT: JAMES, GUY L.
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
; TITLE OF INVENTION: TRANSFERASE INHIBITORS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433

```

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; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,964
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/021,625
; FILING DATE: 16-FEB-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/822,011
; FILING DATE: ABANDONED
; CLASSIFICATION: 435
; APPLICATION NUMBER: PCT/US/91/02650
; FILING DATE: 18-APR-1991
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/615,715
; FILING DATE: 20-NOV-1990
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/510,706
; FILING DATE: 18-APR-1990 (ABANDONED)
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, DAVID L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:432/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0324
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-429-964-15

Query Match 40.5%; Score 30; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 KADNRSC 12
Db 1 RASNRSC 7

RESULT 12
PCT-US93-08062-15
; Sequence 15, Application PC/TUS9308062
; GENERAL INFORMATION:
; APPLICANT:
; SEQUENCE CHARACTERISTICS:
; SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.
; SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.
; SEQUENCE CHARACTERISTICS: REISS, YUVAL
; SEQUENCE CHARACTERISTICS: MARSTERS, JR., JAMES C.
; ADDRESSEE: METHODS AND COMPOSITIONS FOR
; ADDRESSEE: THE IDENTIFICATION
; ADDRESSEE: CHARACTERIZATION AND
; ADDRESSEE: INHIBITION OF
; ADDRESSEE: FARNESYLTRANSFERASE
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433

```

;
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; MEDIUM TYPE: FLOPPY DISK/ASKII
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08062
; FILING DATE: AUGUST 24, 1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/935,087
; FILING DATE: 24 AUGUST 1992 (24.08.92)
; NAME: UNKNOWN
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, DAVID L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTFD377PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; TELEX: NOT APPLICABLE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US93-08062-15

Query Match 40.58; Score 30; DB 5; Length 10;
Best Local Similarity 71.48; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 KADNRSC 12
Db 1 RASNRSC 7

RESULT 13
US-09-100-409A-24
; Sequence 24, Application US/09100409A
; Patent No. 6090388
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION FOR
; PREVENTION AND TREATMENT OF HIV INFECTION AND
; IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,409A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 1151-4154

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-100-409A-24

Query Match 39.28; Score 29; DB 3; Length 12;
Best Local Similarity 33.38; Pred. No. 2.4e+02;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRSMNKADNRSC 12
Db 1 CKGPSKLNDRAC 12

RESULT 14
PCT-US94-01234-71
; Sequence 71, Application PC/TUS9401234
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE
; BINDING SITES
; NUMBER OF SEQUENCES: 76
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01234
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,542
; FILING DATE: 28-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US'08/012,566
; FILING DATE: 02-FEB-1993
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; PCT-US94-01234-71

Query Match 37.88; Score 28; DB 5; Length 11;
Best Local Similarity 40.08; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SMNKADNRSC 12
Db 2 SPQRTDQRNC 11

RESULT 15
US-09-258-754-263
; Sequence 263, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; DIPEPTIDASE
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107

; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 283
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-263

Query Match 37.8%; Score 28; DB 3; Length 12;
Best Local Similarity 41.7%; Pred. No. 3.3e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12
||: ||: ||
Db 1 CRARIRAEIDISC 12

Search completed: August 3, 2005, 12:41:26
Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2005, 12:38:46 ; Search time 152 Seconds
(without alignments)
30.759 Million cell updates/sec

Title: US-09-910-582B-10

Perfect score: 74

Sequence: 1 CRSWNKADNRSC 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 243143

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	74	100.0	12	9	US-09-782-650-5
2	74	100.0	12	10	US-09-910-582B-10
3	74	100.0	12	17	US-10-838-289-38
4	34	45.9	11	9	US-09-912-609-22
5	34	45.9	11	17	US-10-838-289-78
6	32	43.2	11	9	US-09-912-609-25
7	32	43.2	11	17	US-10-838-289-81
8	32	43.2	12	17	US-10-838-289-301
9	32	43.2	12	17	US-10-607-595-244
10	32	43.2	12	18	US-10-492-929-13
11	31	41.9	12	17	US-10-838-289-189
12	41.9				Sequence 5, Appli
13					Sequence 10, Appl
14					Sequence 38, Appl
15					Sequence 28, Appl
16					Sequence 78, Appl
17					Sequence 25, Appl
18					Sequence 81, Appl
19					Sequence 301, App
20					Sequence 244, App
21					Sequence 13, Appl
22					Sequence 189, App

12	41.9	17	US-10-607-595-82	Sequence 82, Appl
13	41.9	18	US-10-492-929-16	Sequence 16, Appl
14	40.5	10	US-09-572-404B-2219	Sequence 2219, Ap
15	40.5	12	US-10-492-929-9	Sequence 9, Appli
16	39.9	11	US-10-398-104-221	Sequence 221, App
17	39.9	12	US-10-363-204-219	Sequence 219, App
18	39.2	5	US-10-714-564A-303	Sequence 303, App
19	39.2	6	US-10-714-564A-304	Sequence 304, App
20	39.2	6	US-10-714-564A-322	Sequence 322, App
21	39.2	7	US-10-714-564A-305	Sequence 305, App
22	39.2	7	US-10-714-564A-323	Sequence 323, App
23	39.2	8	US-10-714-564A-306	Sequence 306, App
24	39.2	8	US-10-714-564A-324	Sequence 324, App
25	39.2	9	US-10-714-564A-307	Sequence 307, App
26	39.2	9	US-10-714-564A-325	Sequence 325, App
27	39.2	10	US-09-572-270A-162	Sequence 162, App
28	39.2	10	US-10-221-993-1	Sequence 1, Appli
29	39.2	10	US-10-714-564A-308	Sequence 308, App
30	39.2	10	US-10-714-564A-326	Sequence 326, App
31	39.2	11	US-09-912-609-24	Sequence 24, Appl
32	39.2	11	US-10-714-564A-309	Sequence 309, App
33	39.2	11	US-10-714-564A-327	Sequence 327, App
34	39.2	11	US-10-838-289-80	Sequence 80, Appl
35	39.2	12	US-10-607-595-263	Sequence 263, App
36	39.2	12	US-10-190-082-556	Sequence 556, App
37	39.2	12	US-10-714-564A-310	Sequence 310, App
38	39.2	12	US-10-714-564A-328	Sequence 328, App
39	37.8	9	US-10-777-053-378	Sequence 378, App
40	37.8	9	US-10-837-217-378	Sequence 378, App
41	37.8	11	US-09-912-609-27	Sequence 27, Appl
42	37.8	11	US-10-838-289-83	Sequence 83, Appl
43	37.8	12	US-10-838-289-320	Sequence 320, App
44	37.2	9	US-10-046-922-62	Sequence 62, Appl
45	37.2	9	US-10-363-205-162	Sequence 162, App
46	36.5	7	US-10-727-335-79	Sequence 79, Appl
47	36.5	9	US-09-832-723-94	Sequence 94, Appl
48	36.5	9	US-09-938-864-49	Sequence 49, Appl
49	36.5	9	US-09-938-864-131	Sequence 131, App
50	36.5	9	US-09-938-864-167	Sequence 167, App
51	36.5	9	US-09-938-864-258	Sequence 258, App
52	36.5	9	US-09-938-864-278	Sequence 278, App
53	36.5	9	US-09-791-477-49	Sequence 49, Appl
54	36.5	9	US-09-791-477-131	Sequence 131, App
55	36.5	9	US-09-791-477-167	Sequence 167, App
56	36.5	9	US-09-791-477-258	Sequence 258, App
57	36.5	9	US-09-791-477-278	Sequence 278, App
58	36.5	9	US-09-785-019-49	Sequence 49, Appl
59	36.5	9	US-09-785-019-131	Sequence 131, App
60	36.5	9	US-09-785-019-167	Sequence 167, App
61	36.5	9	US-09-785-019-258	Sequence 258, App
62	36.5	9	US-10-125-635A-49	Sequence 49, Appl
63	36.5	9	US-10-125-635A-131	Sequence 131, App
64	36.5	9	US-10-125-635A-167	Sequence 167, App
65	36.5	9	US-10-125-635A-258	Sequence 258, App
66	36.5	9	US-10-125-635A-278	Sequence 278, App
67	36.5	9	US-10-002-603-49	Sequence 49, Appl
68	36.5	9	US-10-002-603-131	Sequence 131, App
69	36.5	9	US-10-002-603-167	Sequence 167, App
70	36.5	9	US-10-002-603-258	Sequence 258, App
71	36.5	9	US-10-002-603-278	Sequence 278, App
72	36.5	9	US-10-303-331-94	Sequence 94, Appl
73	36.5	9	US-10-195-835-49	Sequence 49, Appl
74	36.5	9	US-10-195-835-131	Sequence 131, App
75	36.5	9	US-10-195-835-167	Sequence 167, App
76	36.5	9	US-10-195-835-258	Sequence 258, App
77	36.5	9	US-10-195-835-278	Sequence 278, App
78	36.5	9	US-10-286-333-49	Sequence 49, Appl
79	36.5	9	US-10-286-333-131	Sequence 131, App
80	36.5	9	US-10-286-333-167	Sequence 167, App
81	36.5	9	US-10-286-333-258	Sequence 258, App
82	36.5	9	US-10-286-333-278	Sequence 278, App
83	36.5	9	US-10-244-830-49	Sequence 49, Appl

85 27 36.5 9 15 US-10-244-830-131 Sequence 131, App
86 27 36.5 9 15 US-10-244-830-167 Sequence 167, App
87 27 36.5 9 15 US-10-244-830-258 Sequence 258, App
88 27 36.5 9 15 US-10-244-830-278 Sequence 278, App
89 27 36.5 9 15 US-10-427-717-49 Sequence 49, Appl
90 27 36.5 9 15 US-10-427-717-131 Sequence 131, App
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93 27 36.5 9 15 US-10-427-717-278 Sequence 278, App
94 27 36.5 9 15 US-10-471-835-2 Sequence 2, Appl
95 27 36.5 9 16 US-10-648-780-49 Sequence 49, Appl
96 27 36.5 9 16 US-10-648-780-131 Sequence 131, App
97 27 36.5 9 16 US-10-648-780-167 Sequence 167, App
98 27 36.5 9 16 US-10-648-780-258 Sequence 258, App
99 27 36.5 9 16 US-10-648-780-278 Sequence 278, App
100 27 36.5 9 16 US-10-490-873-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-782-650-5
; Sequence 5, Application US/09782650
; Patent No. US20020019350A1
; GENERAL INFORMATION:
; APPLICANT: Levine, Arnold J.
; APPLICANT: Mitterer, Artur
; APPLICANT: Falkner, Falko-Guenter
; APPLICANT: Scheiflinger, Friedrich
; APPLICANT: Dörner, Friedrich
; APPLICANT: Edwards Lifesciences Corporation
; TITLE OF INVENTION: Targeted Angiogenesis
; FILE REFERENCE: 20553D-000611US
; CURRENT APPLICATION NUMBER: US/09/782,650
; CURRENT FILING DATE: 2001-02-12
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 09/324,079
; PRIOR FILING DATE: 1999-06-07
; PRIOR APPLICATION NUMBER: US 09/327,045
; PRIOR FILING DATE: 1999-06-07
; PRIOR APPLICATION NUMBER: PCT/US00/14988
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:targeting
; OTHER INFORMATION: molecule
US-09-782-650-5

Query Match 100.0%; Score 74; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRSWNKADNRSC 12
Db 1 CRSWNKADNRSC 12
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RESULT 2
US-09-910-582b-10
; Sequence 10, Application US/09910582B
; Publication No. US20030045476A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Mackenna, Deirdre A.
; TITLE OF INVENTION: Heart Homing Conjugates
; FILE REFERENCE: P-LJ 4857
; CURRENT APPLICATION NUMBER: US/09/910,582B
; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 09/326,718
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-910-582b-10

Query Match 100.0%; Score 74; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRSWNKADNRSC 12
Db 1 CRSWNKADNRSC 12
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RESULT 3
US-10-838-289-38
; Sequence 38, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jimming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; FILE REFERENCE: CRRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Heart homing peptide
US-10-838-289-38

Query Match 100.0%; Score 74; DB 17; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRSWNKADNRSC 12
Db 1 CRSWNKADNRSC 12
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RESULT 4
US-09-912-609-22
; Sequence 22, Application US/09912609
; Publication No. US20020041898A1
; GENERAL INFORMATION:
; APPLICANT: UNGER, EVAN C.
; APPLICANT: MATSUNAGA, TERRY ONICHI
; APPLICANT: RAMASWAMI, VARADARAJAN
; APPLICANT: ROMANOWSKI, MAREK J.
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 5030-0001-24
; CURRENT APPLICATION NUMBER: US/09/912,609
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 09/703,474
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/478,124
; PRIOR FILING DATE: 2000-01-05

; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-912-609-22

Query Match 45.9%; Score 34; DB 9; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 SWNKADNRSC 12
| : | | | |
Db 2 SFGKGNRIC 11

RESULT 5
US-10-838-289-78
; Sequence 78, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jinming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; TITLE OF INVENTION: NANOSHELLS
; FILE REFERENCE: CWRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: RGD-binding determinant homing peptide
US-10-838-289-78

Query Match 45.9%; Score 34; DB 17; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 SWNKADNRSC 12
| : | | | |
Db 2 SFGKGNRIC 11

RESULT 6
US-09-912-609-25
; Sequence 25, Application US/09912609
; Publication No. US20020041898A1
; GENERAL INFORMATION:
; APPLICANT: UNGER, EVAN C.
; APPLICANT: MATSUNAGA, TERRY ONICHI
; APPLICANT: RAMASWAMI, VARADARAJAN
; APPLICANT: ROMANOWSKI, MAREK J.
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 5030-0001.24
; CURRENT APPLICATION NUMBER: US/09/912,609
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 09/703,474
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/478,124
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 131

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-912-609-25

Query Match 43.2%; Score 32; DB 9; Length 11;
Best Local Similarity 50.0%; Pred. No. 3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 SWNKADNRSC 12
| : | | | |
Db 2 SFGGRDRNC 11

RESULT 7
US-10-838-289-81
; Sequence 81, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jinming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; TITLE OF INVENTION: NANOSHELLS
; FILE REFERENCE: CWRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: RGD-binding determinant homing peptide
US-10-838-289-81

Query Match 43.2%; Score 32; DB 17; Length 11;
Best Local Similarity 50.0%; Pred. No. 3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 SWNKADNRSC 12
| : | | | |
Db 2 SFGGRDRNC 11

RESULT 8
US-10-838-289-301
; Sequence 301, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jinming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; TITLE OF INVENTION: NANOSHELLS
; FILE REFERENCE: CWRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 301

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; LENGTH: 12
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Retina homing peptide
US-10-838-289-301

Query Match          43.2%; Score 32; DB 17; Length 12;
Best Local Similarity 41.7%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 CRSWNKADNRSC 12
      | : | : |
Db      1 QQRVSVENASC 12

RESULT 9
US-10-607-595-244
; Sequence 244, Application US/10607595
; Publication No. US20050074812A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/10/607,595
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/722,250
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 244
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-607-595-244

Query Match          43.2%; Score 32; DB 17; Length 12;
Best Local Similarity 41.7%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 CRSWNKADNRSC 12
      | : | : |
Db      1 QQRVSVENASC 12

RESULT 10
US-10-492-929-13
; Sequence 13, Application US/10492929
; Publication No. US20050124544A1
; GENERAL INFORMATION:
; APPLICANT: GRANIER, CLAUDE
; APPLICANT: VILLARD, SYLVIE
; TITLE OF INVENTION: PEPTIDE DECOYS FOR THE PREPARATION OF MEDICAMENTS
; TITLE OF INVENTION: INTENDED FOR THE PREVENTION OR TREATMENT OF AUTOIMMUNE
; TITLE OF INVENTION: PATHOLOGIES, OR DISORDERS LINKED TO THE APPEARANCE OF
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST EXOGENOUS PROTEINS
; FILE REFERENCE: 0508-1103
; CURRENT APPLICATION NUMBER: US/10/492,929
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: PCT/FR02/03557
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: FR 01/13360
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 12
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-492-929-13

Query Match          43.2%; Score 32; DB 18; Length 12;
Best Local Similarity 33.3%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY      1 CRSWNKADNRSC 12
      | : | : |
Db      1 CSKWHNRSKRHC 12

RESULT 11
US-10-838-289-189
; Sequence 189, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jimming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; FILE REFERENCE: CWRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Lung homing peptide
US-10-838-289-189

Query Match          41.9%; Score 31; DB 17; Length 12;
Best Local Similarity 33.3%; Pred. No. 4.6e+02;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      1 CRSWNKADNRSC 12
      | : | : |
Db      1 CRPHNQAHTEC 12

RESULT 12
US-10-607-595-82
; Sequence 82, Application US/10607595
; Publication No. US20050074812A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/10/607,595
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/722,250
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-607-595-82

Query Match 41.9%; Score 31; DB 17; Length 12;
Best Local Similarity 33.3%; Pred. No. 4.6e+02;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 CRSWNKADNRSC 12
| : | : | : |
Db 1 CRPHNQAHTEC 12

RESULT 13
US-10-492-929-16
; Sequence 16, Application US/10492929
; Publication No. US20050124544A1
; GENERAL INFORMATION:
; APPLICANT: GRANIER, CLAUDE
; TITLE OF INVENTION: PEPTIDE DECOYS FOR THE PREPARATION OF MEDICAMENTS
; TITLE OF INVENTION: INTENDED FOR THE PREVENTION OR TREATMENT OF AUTOIMMUNE
; TITLE OF INVENTION: PATHOLOGIES, OR DISORDERS LINKED TO THE APPEARANCE OF
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST EXOGENOUS PROTEINS
; FILE REFERENCE: 0508-1103
; CURRENT APPLICATION NUMBER: US/10/492,929
; PRIOR FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: PCT/FR02/03557
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: FR 01/13360
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-492-929-16

Query Match 41.9%; Score 31; DB 18; Length 12;
Best Local Similarity 33.3%; Pred. No. 4.6e+02;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 CRSWNKADNRSC 12
| : | : | : |
Db 1 CMKWSNRSSWC 12

RESULT 14
US-09-572-404B-2219
; Sequence 2219, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2219
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in C7 at 702-711 and may interact with Sequence
; OTHER INFORMATION: this patent.
US-09-572-404B-2219

Query Match 40.5%; Score 30; DB 10; Length 10;

Best Local Similarity 44.4%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRSWNKADN 9
| : | : | : |
Db 1 CORWEKLQN 9

RESULT 15
US-10-492-929-9
; Sequence 9, Application US/10492929
; Publication No. US20050124544A1
; GENERAL INFORMATION:
; APPLICANT: GRANIER, CLAUDE
; APPLICANT: VILLARD, SYLVIE
; TITLE OF INVENTION: PEPTIDE DECOYS FOR THE PREPARATION OF MEDICAMENTS
; TITLE OF INVENTION: INTENDED FOR THE PREVENTION OR TREATMENT OF AUTOIMMUNE
; TITLE OF INVENTION: PATHOLOGIES, OR DISORDERS LINKED TO THE APPEARANCE OF
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST EXOGENOUS PROTEINS
; FILE REFERENCE: 0508-1103
; CURRENT APPLICATION NUMBER: US/10/492,929
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: PCT/FR02/03557
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: FR 01/13360
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-492-929-9

Query Match 40.5%; Score 30; DB 18; Length 12;
Best Local Similarity 41.7%; Pred. No. 6.5e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 1 CRSWNKADNRSC 12
| : | : | : |
Db 2 CHTW--SNRRSC 11

Search completed: August 3, 2005, 12:53:14
Job time : 153 secs

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